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FIGURE 1

CTAAAAAATATGTTCTCTACAACACCAAGGCTCATTAAAATATTTTAAATATT
AATATACATTTCTTCTGTCAGAAATACATAAAACTTTATTATATCAGCGCAGG
GCGGCGCGGCGTCCGTCGGTCCCGGGAGCAGAACCCGGCTTTTTCTTGGAGCGACG
CTGTCTCTAGTCGCTGATCCCAAATGCACCGGCTCATCTTTGTCTACACTCTA
ATCTGCGCAAACCTTTTGCAGCTGTCTGGGACACTTCTGCAACCCCGCAGAGCG
CATCCATCAAAGCTTTGCGCAACGCCAACCTCAGGCGAGATGAGAGCAATCA
CCTCACAGACTTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGG
CTACGTGCAGAGTCCTAGATTCCCGAACAGCTACCCCGAGGAACCTGCTCCTG
ACATGGCGGCTTCACTCTCAGGAGAATACACGGATACAGCTAGTGTGTTGACA
ATCAGTTTGGATTAGAGGAAGCAGAAAATGATATCTGTAGGTATGATTTTGT
GGAAGTTGAAGATATATCCGAAACCAGTACCATTATTAGAGGACGATGGTGT
GGACACAAGGAAGTTCCCTCCAAGGATAAAATCAAGAACGAACCAAATTA
ATCACATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGATT
TTATTCTTTGCTGGAAGATTTCCAACCCGCAGCAGCTTCAGAGACCAACTGGG
AATCTGTCACAAGCTCTATTTCAAGGGGTATCCTATAACTCTCCATCAGTAACG
GATCCCACTCTGATTGCGGATGCTCTGGACAAAAAAATTGCAGAATTTGATA
CAGTGGAAGATCTGCTCAAGTACTTCAATCCAGAGTCATGGCAAGAAGATCT
TGAGAATATGTATCTGGACACCCCTCGGTATCGAGGCAGGTCATACCATGAC
CGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCGTTACA
GTTGCACTCCCAGGAATTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGGC
CAATGTGGTCTTCTTTCCACGTTGCCTCCTCGTGCAGCGCTGTGGAGGAAATT
GTGGCTGTGGAAGTGTCAACTGGAGGTCCTGCACATGCAATTCAGGGAAAAC
CGTGAAAAAGTATCATGAGGTATTACAGTTTGAGCCTGGCCACATCAAGAGG
AGGGGTAGAGCTAAGACCATGGCTCTAGTTGACATCCAGTTGGATCACCATG
AACGATGTGATTGTATCTGCAGCTCAAGACCACCTCGATAAGAGAATGTGCA
CATCCTTACATTAAGCCTGAAAGAACCCTTTAGTTTAAGGAGGGTGAGATAAG
AGACCCTTTTCTACCAGCAACCAAACCTTACTACTAGCCTGCAATGCAATGA
ACACAAGTGGTTGCTGAGTCTCAGCCTTGCTTTGTTAATGCCATGGCAAGTAG
AAAGGTATATCATCAACTTCTATACCTAAGAATATAGGATTGCATTTAATAAT
AGTGTGTTGAGGTTATATATGCACAAACACACACAGAAATATATTCATGTCTAT
GTGTATATAGATCAAATGTTTTTTTTGGTATATATAACCAGGTACACCAGAGC
TTACATATGTTTGAGTTAGACTCTTAAATCCTTTGCCAAAATAAGGGATGGT
CAAATATATGAAACATGTCTTTAGAAAATTTAGGAGATAAATTTATTTTAAA
TTTTGAAACACAAAACAATTTTGAATCTTGCTCTCTTAAAGAAAGCATCTTGT
ATATTAAAAATCAAAGATGAGGCTTCTTACATATACATCTTAGTTG (SEQ
ID NO:50)



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Figure 2A

1 CTAAAAAATATGTTCTCTACACACCAAGGCTCATTAAAAATATTT
46 TAAATATTAAATATACATTTTCTTCTGTGTCAGAAATACATAAACTTT
5 91 ATTATATCAGCGCAGGGCGGGCGCGCGTCCGGTCCCGGGAGCAGAA
136 CCCGGCTTTTCTTGGAGCGACGCTGTCTCTAGTCGCTGATCCCA

181 AATGCACCGGCTCATCTTTGTCTACACTCTAATCTGCGCAAACCTT
MetHisArgLeuIlePheValTyrThrLeuIleCysAlaAsnPhe
10 226 TTGCAGCTGTCCGGACACTTCTGCAACCCCGCAGAGCGCATCCAT
CysSerCysArgAspThrSerAlaThrProGlnSerAlaSerIle

271 CAAAGCTTTGCGCAACGCCAACCTCAGGCGAGATGAGAGCAATCA
15 LysAlaLeuArgAsnAlaAsnLeuArgArgAspGluSerAsnHis

316 CCTCACAGACTTGTACCGAAGAGATGAGACCATCCAGGTGAAAGG
LeuThrAspLeuTyrArgArgAspGluThrIleGlnValLysGly

20 361 AAACGGCTACGTGCAGAGTCCTAGATTCCCGAACAGCTACCCAG
AsnGlyTyrValGlnSerProArgPheProAsnSerTyrProArg

406 GAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAATACAG
AsnLeuLeuLeuThrTrpArgLeuHisSerGlnGluAsnThrArg
25 451 GATACAGCTAGTGTGTTGACAATCAGTTTGGATTAGAGGAAGCAGA
IleGlnLeuValPheAspAsnGlnPheGlyLeuGluGluAlaGlu

496 AAATGATATCTGTAGGTATGATTTTGTGGAAGTTGAAGATATATC
30 AsnAspIleCysArgTyrAspPheValGluValGluAspIleSer

541 CGAAACCAGTACCATTATTAGAGGACGATGGTGTGGACACAAGGA
GluThrSerThrIleIleArgGlyArgTrpCysGlyHisLysGlu

35 586 AGTTCCTCCAAGGATAAAATCAAGAACGAACCAAATTAAATCAC
ValProProArgIleLysSerArgThrAsnGlnIleLysIleThr

631 ATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGAT



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Figure 2B

PheLysSerAspAspTyrPheValAlaLysProGlyPheLysIle

676 TTATTATTCTTTGCTGGAAGATTTCCAACCCGACGAGCTTCAGA
TyrTyrSerLeuLeuGluAspPheGlnProAlaAlaAlaSerGlu721 GACCAACTGGGAATCTGTCAAGCTCTATTTAGGGGTATCCTA
ThrAsnTrpGluSerValThrSerSerIleSerGlyValSerTyr766 TAACTCTCCATCAGTAACGGATCCCACTCTGATTGCGGATGCTCT
AsnSerProSerValThrAspProThrLeuIleAlaAspAlaLeu811 GGACAAAAAATTGCAGAATTGATACAGTGAAGATCTGCTCAA
AspLysLysIleAlaGluPheAspThrValGluAspLeuLeuLys856 GTACTTCAATCCAGAGTCATGGCAAGAAGATCTTGAGAATATGTA
TyrPheAsnProGluSerTrpGlnGluAspLeuGluAsnMetTyr901 TCTGGACACCCCTCGGTATCGAGGCAGGTCATACCATGACCGGAA
LeuAspThrProArgTyrArgGlyArgSerTyrHisAspArgLys946 GTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCGTTA
SerLysValAspLeuAspArgLeuAsnAspAspAlaLysArgTyr991 CAGTTGCACTCCAGGAATTACTCGGTCAATATAAGAGAAGAGCT
SerCysThrProArgAsnTyrSerValAsnIleArgGluGluLeu1036 GAAGTTGGCCAATGTGGTCTTCTTTCCACGTTGCCTCCTCGTGCA
LysLeuAlaAsnValValPhePheProArgCysLeuLeuValGln1081 GCGCTGTGGAGGAAATTGTGGCTGTGGAAGTGTCAACTGGAGGTC
ArgCysGlyGlyAsnCysGlyCysGlyThrValAsnTrpArgSer1126 CTGCACATCAATTCAAGGAAAACCGTGAAAAAGTATCATGAGGT
CysThrCysAsnSerGlyLysThrValLysLysTyrHisGluVal1171 ATTACAGTTTGAGCCTGGCCACATCAAGAGGAGGGGTAGAGCTAA
LeuGlnPheGluProGlyHisIleLysArgArgGlyArgAlaLys



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Figure 2C

1216 GACCATGGCTCTAGTTGACATCCAGTTGGATCACCATGAACGATG
ThrMetAlaLeuValAspIleGlnLeuAspHisHisGluArgCys

5

1261 TGATTGTATCTGCAGCTCAAGACCACCTCGATAAGAGAATGTGCA
AspCysIleCysSerSerArgProProArg (SEQ ID NO:12)

10

1306 CATCCTTACATTAAGCCTGAAAGAACCTTTAGTTTAAGGAGGGTG
1351 AGATAAGAGACCCCTTTTCCTACCAGCAACCAAACCTTACTACTAGC
1396 CTGCAATGCAATGAACACAAGTGGTTGCTGAGTCTCAGCCTTGCT
1441 TTGTTAATGCCATGGCAAGTAGAAAGGTATATCATCAACTTCTAT
1486 ACCTAAGAATATAGGATTGCATTTAATAATAGTGTGAGGTTAT
1531 ATATGCACAAACACACACAGAAATATATTCATGTCTATGTGTATA

15

1576 TAGATCAAATGTTTTTTTTTGGTATATATAACCAGGTACACCAGAG
1621 CTTACATATGTTTGGAGTTAGACTCTTAAAATCCTTTGCCAAAATA
1666 AGGGATGGTCAAATATATGAAACATGTCTTTAGAAAATTTAGGAG
1711 ATAAATTTATTTTTAAATTTTGAAACACAAAACAATTTGAATCT
1756 TGCTCTCTTAAAGAAAGCATCTTGTATATTAAAAATCAAAGATG
1801 AGGCTTTCTTACATATACATCTTAGTTG (SEQ ID NO:50)



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FIGURE 3

A -- Cur2 1.6 heavy chain nucleotide sequence

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCC
TGAGACTCTCCTGTGCAGCCTCTGGATTCAACTTCAGAACCTATAACATGAAC
TGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCATCCATTAGTA
GTAGTAGTAGTAACATATACTACGCAGACTCAGTGAAGGGCCGATTACCCAT
CTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAACAGCCTGAGA
GCCGAGGACACGGCTGTATATTACTGTGCGAGAGATATTATGATTACGTTTG
GGGGAATTATCGCCTCGTTCTACTTTGACTACTGGGGCCAGGGAACCCTGGTC
ACCGTCTCCTCAG (SEQ ID NO:55)

B -- Cur2 1.6 heavy chain amino acid sequence

EVQLVESGGGLVKPGGSLRLSCAASGFNFRITYNMNWVRQAPGKGLEWVSSISS
SSNIYYADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCARDIMITFGGIIAS
FYFDYWGQGLVTVSS (SEQ ID NO:13)

C -- Cur2 1.6 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
TTTCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCCA
GTTTGCAAAGTGGGGTCCCATCAAGGTTCAAGCGGCAGTGGATCTGGGACAGA
ATTCATCTCACAAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT
GTCTACAGCATAATAGTTACCCGCTCACTTTCGGCGGAGGGACCAAGGTGGA
GATCAAAC (SEQ ID NO:56)

D -- Cur2 1.6 light chain amino acid sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWFQKPGKAPKRLIYAASSLQ
SGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGGTKVEIK (SEQ
ID NO:14)



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FIGURE 4

A -- Cur2 1.11 heavy chain nucleotide sequence

GAGGTGCAGCTGGTGCAGTCTGGAGGAGGCTTGATCCAGCCTGGGGGGTCCC
TGAGACTCTCCTGTGCAGCCTCTGGGTTACACGTCAGTAGCAACTACATGAGC
TGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGTTATTTATA
GCGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGATTACCATCTC
CAGAGACAATTCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCC
GAGGACACGGCCGTGTATTACTGTGCGGGAACGGTGACTACGAATTACTACT
ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAG (SEQ
ID NO:57)

B -- Cur2 1.11 heavy chain amino acid sequence

EVQLVQSGGGLIQPGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVIYSG
GSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAGTVTTNYYYGM
DVWGQGTTVTVSS (SEQ ID NO:15)

C -- Cur2 1.11 light chain nucleotide sequence

GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCC
GGCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCAAAGTAATGGATAC
AACTATTTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGA
TCTATTTGGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGGTTTCAGTGGCAGT
GGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATG
TTGGGGTTTATTACTGCATGCAAGCTCTACAACTCTCACTTTCGGCGGAGGG
ACCAAGGTGGAGATCAAAC (SEQ ID NO:58)

D -- Cur2 1.11 light chain amino acid sequence

DIVMTQSPLSLPVTPGEPASISCRSSQSLQSNQYNYLDWYLQKPGQSPQLLIYLG
SNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTLTFGGGTKVEI
K (SEQ ID NO:16)



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FIGURE 5

A -- Cur2 1.17 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGGAGTCGGGGGGAGGCGTGGTCCAGCCTGGGAAGTCCC
TGAGACTCTCCTGTGCAGCGTCTGGATTACCTTCAGTAGCTATGGCATGCAC
TGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGT
ATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTACCAT
CTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGA
GCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCAAGGATACAGATATG
CTGGTTACTACTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGT
CACCGTCTCCTCAG (SEQ ID NO:59)

B -- Cur2 1.17 heavy chain protein sequence

QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIW
YDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDQGYRYA
GYYYDYGMDVWGQGTTVTVSS (SEQ ID NO:17)

C -- Cur2 1.17 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
TATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCCA
GTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGA
ATTCATCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT
GTCTACAGCATAATAGTTACCCGCTCACTTTCGGCGGAGGGACCAAGGTGGA
GATCAAAC (SEQ ID NO:60)

D -- Cur2 1.17 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ
SGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK (SEQ
ID NO:18)



FIGURE 6

A -- Cur2 1.18 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGCAGTCGGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA
GTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAGTTATGATATCAA
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATGAA
CCCAAACAGTGGTAACACAGGCTATGCACAGAAGTTCAGGGCAGAGTCACC
ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA
GATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGAGGGTATAGCAGTGGC
TGGGACATACTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACG
GTCACCGTCTCCTCAG (SEQ ID NO:61)

B -- Cur2 1.18 heavy chain protein sequence

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWM
NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDVAVYYCAREGIAVAG
TYYYYYGMVDVWGQGTITVTVSS (SEQ D NO:19)

C -- Cur2 1.18 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
TATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCCA
GTTTGCAAAGTGGGGTCCCATCAAGGTTCAAGCGGCAGTGGATCTGGGACAGA
ATTCATCTCACAAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTTCT
GTCTACAGCATAATAGTTACCCATTCATTTTCGGCCCTGGGACCAAAGTGGAT
ATCAAAC (SEQ ID NO:62)

D -- Cur2 1.18 light chain protein sequence

DIQMTQSPSSLSASVGDRTTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ
SGVPSRFSGSGSGTEFTLTISLQPEDFATYFCLQHNSYPFTFGPGTKVDIK (SEQ
ID NO:20)



FIGURE 7

A -- Cur2 1.19 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAG
TGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAGTTATGATATCAAC
TGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATGAAC
CCTAACAGTGGTAACACAGGCTATGCACAGAAGTTCCAGGGCAGAGTCACCA
TGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGAG
ATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACGTTATGATTACGTTTG
GGGGAGTTATCGTGCCTACGGTATGGACGTCTGGGGCCAAGGGACCACGGT
CACCGTCTCCTCAG (SEQ ID NO:63)

B -- Cur2 1.19 heavy chain amino acid sequence

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWM
NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDVAVYYCARDVMITFG
GVIVHYGMDVWGQGTITVTVSS (SEQ ID NO:21)

C -- Cur2 1.19 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
TATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCCA
GTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGA
TTTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT
GTCTACAGCATAATAGTGACCCGTGCAGTTTTGGCCAGGGGACCAAGCTGGA
GATCAGAC (SEQ ID NO:64)

D -- Cur2 1.19 light chain amino acid sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ
SGVPSRFSGSGSGTDFTLTISLQPEDFATYYCLQHNSDPCSFGQGTKLEIR (SEQ
ID NO:22)



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FIGURE 8

A -- Cur2 1.23 heavy chain nucleotide sequence

GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCT
CTGAAGATCTCCTGTGAGGGTTCTGGATACAGCTTTACCAGCTACTGGATCGG
CTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATCATCTAT
CCTGGTGACTCTGATACCAGATACAGCCCGTCCTTCCAAGGCCAGGTCACCA
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA
GGCCTCGGACACCGCCATGTATTACTGTGCGAGACATGTATCGTATTACTATG
TTTCGGGGAGTTATTATAACGTCTTTGACTACTGGGGCCAGGGAACCCTGGTC
ACCGTCTCCTCAG (SEQ ID NO:65)

B -- Cur2 1.23 heavy chain amino acid sequence

EVQLVQSGAEVKKPGESLKISCEGSGYSFTSYWIGWVRQMPGKGLEWMGIYPG
DSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARHVSYYYVSGS
YYNVFDYWGGQTLVTVSS (SEQ ID NO:23)

C -- Cur2 1.23 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
TATCAGCAGATACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCCA
GTTTGCAACGTGGGGTCCCATCAAGGTTCAAGCGCAGTGGATCTGGGACAGA
ATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT
GTCTACAGCATAATAGTTACCCGTGGACGTTTCGGCCAAGGGACCAAGGTGGA
AATCAAAC (SEQ ID NO:66)

D -- Cur2 1.23 light chain amino acid sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQIPGKAPKRLIYAASSLQR
GVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPWTFGQGKVEIK (SEQ
ID NO:24)



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FIGURE 9

A -- Cur2 1.24.1 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCC
TGAGACTCTCCTGTGCAGCGTCTGGATTTCAGTTTCAGTAGCTATGGCATGCAC
TGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGATATATGGT
ATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCAT
CTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGA
GCCGAGGACACGGCTGTGTATTATTGTGCGAGAGATCAGGGGATACAGCTATG
GTTACGTCTACTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGT
CACCGTCTCCTCAG (SEQ ID NO:67)

B -- Cur2 1.24.1 heavy chain protein sequence

QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQAPGKGLEWVADIW
YDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLR AEDTAVYYCARDQGY SYG
YVYYDYGMDVWGQGT VTVSS (SEQ ID NO:25)

C -- Cur2 1.24.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
TATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCCA
GTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGA
GTTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT
GTCTACAGCATAATAGTTACCCGTGGACGTTTCGGCCAAGGGACCAAGGTGGA
AATCAAAC (SEQ ID NO:68)

D -- Cur2 1.24.1 light chain protein sequence

DIQMTQSPSSLSASVGDRVITICRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ
SGVPSRFSGSGSTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK (SEQ
ID NO:26)



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FIGURE 10

A -- Cur2 1.25.1 heavy chain nucleotide sequence

GAGGTGCAGCTGGTGCAGTCGGGAGCAGAGGTGAAAAAGCCCGGGGAGTCT
CTGAAGATCTCCTGTAAGGGTTCTGGATACAGGTTTACCAGCTACTGGATCGG
CTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATCATCTAT
CCTGGTGACTCTGATACCAGATACAGCCCGTCCTTCCAAGGCCAGGTCACCA
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA
GGCCTCGGACACCGCCATGTATTACTGTGCGAGACATGGATCGTATTATTATG
GTTCCGAGACTTATTATAATGTCTTTGACTACTGGGGCCAGGGAACCCTGGTC
ACCGTCTCCTCAG (SEQ ID NO:69)

B -- Cur2 1.25.1 heavy chain protein sequence

EVQLVQSGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGHIYPG
DSDTRYSPSFQGGQVTISADKSISTAYLQWSSLKASDTAMYICARHGSYYYGSET
YYNVFDYWGGQGLTVTVSS (SEQ ID NO:27)

C -- Cur2 1.25.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
TATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCCA
GTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGA
ATTCATCTCACAAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT
GTCTACAGCATAATAGTTACCCGTGGACGTTTCGGCCAAGGGACCAAGGTGGA
AATCAAAC (SEQ ID NO:70)

D -- Cur2 1.25.1 light chain protein sequence

DIQMTQSPSSLSASVGDRTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ
SGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPWTFGQGTKVEIK (SEQ
ID NO:28)



FIGURE 11

A -- Cur2 1.29 heavy chain nucleotide sequence

GAGGTGCAGCTGGTGCAGTCGGGAGCAGAGGTGAAAAAGCCCCGGGGAGTCT
CTGAAGATCTCCTGTAAGGGTTCTGGATACAGCTTTACCAGCTACTGGATCGG
CTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATCATCTAT
CCTGGTGACTCTGATACCAGATACAGCCCGTCCTTCCAAGGCCAGGCCACCA
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA
GGCCTCGGACACCGCCATGTATTACTGTGCGAGACACGTGGATGTAGGGGCT
ACGATTGGGGGATATTACTATTACTACCACGGTATGGACGTCTGGGGCCAAG
GGACCACGGTCACCGTCTCCTCAG (SEQ ID NO:71)

B -- Cur2 1.29 heavy chain protein sequence

EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIHYPG
DSDTRYSPSFQGQATISADKSISTAYLQWSSLKASDTAMYCARHVDVGATIGG
YYYYYHGMDVWGQGTTVTVSS (SEQ ID NO:29)

C -- Cur2 1.29 light chain nucleotide sequence

GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCC
GGCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACA
ACTATTTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAACCTCCTGATC
TATTTGGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGGTTCACTGGCAGTGG
ATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGGCTGACGATGTT
GGGGTTTATTACTGCATGCAAGCTCTACAATCTCTCATGTGCAGTTTGGCCA
GGGGACCAAGCTGGAGATCAAAC (SEQ ID NO:72)

D -- Cur2 1.29 light chain protein sequence

DIVMTQSPLSLPVTPGEPASISCRSSQSLLSNGYNYLDWYLQKPGQSPQLLIYLG
SNRASGVPRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTL
EIK (SEQ ID NO:30)



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FIGURE 12

A -- Cur2 1.33 heavy chain nucleotide sequence

CAGGTTTCAGCTGGTGCAGTCGGGAGCTGAGGTGAAGAAGCCTGGGGCCTCAG
TGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTTACCAGCTATGGTATCAGC
TGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCAGCG
CTTACAATGGTAACACAAACTATGCACAGAAGCTCCAGGGCAGAGTCACCAT
GACCACAGACACATCCACGAGCACAGCCTACATGGAGCTGAGGAGCCTGAG
ATCTGACGACACGGCCGTGTATTACTGTGCGAGAGATCATTACTATGATAGT
AGTGATTATCTCTACTACTACTACGGTTTGGACGTCTGGGGCCAAGGGACCAC
GGTCACCGTCTCCTCAG (SEQ ID NO:73)

B -- Cur2 1.33 heavy chain protein sequence

QVQLVQSGAEVKKPGASVKVSKASGYTFTSYGISWVRQAPGQGLEWMGWISA
YNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDHYDSS
DYLYYYYGLDVWGQGTTVTVSS (SEQ ID NO:31)

C -- Cur2 1.33 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGT
ATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCAC
TTTGCAATCAGGGGTCCCATCTCGGTTCAAGTGGCAGTGGATCTGGGACAGATT
TCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGT
CAAAAGTATAACAGTGCCCCGCTCACTTTCGGCGGAGGGACCAAGGTGGAGA
TCAAAC (SEQ ID NO:74)

D -- Cur2 1.33 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASLTQ
SGVPSRFSGSGSGTDFTLTISLQPEDVATYYCQKYNAPLTFGGGTKVEIK (SEQ
ID NO:32)



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FIGURE 13

A -- Cur2 1.38.1 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGGAGTCGGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCC
TGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCAC
TGGGTCCGCCAGGCTCCAGGCAAGGGGGCTGGAGTGGGTGGCAATTATATGGT
ATGATGGAAATGATAAATACTATGCAGACTCCGTGAAGGGCCGCTTCACCGT
CTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGA
GCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGATATTACTATGATAGTA
GTGATTATCTCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCAC
GGTCACCGTCTCCTCAG (SEQ ID NO:75)

B -- Cur2 1.38.1 heavy chain protein sequence

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAIIWY
DGNDKYYADSVKGRFTVSRDNSKNTLYLQMNSLRAEDTAVYYCARGYYYDSS
DYLYYYYGMDVWGQGTTVTVSS (SEQ ID NO:33)

C -- Cur2 1.38.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGT
ATCAGCAGAAACCAGGGAAAGTTCCTAACCTCCTGATCTATGCTGCATCCAC
TTTGCAATCAGGGGTCCCATCTCGGTTCAGTGGCAGTGGATCTGGGACAGATT
TCTCTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAGCTTATTACTGT
CAAAAGTGTAACAGTGCCCCGTGGACGTTCCGGCCAAGGGACCACGGTGGAG
ATCAAAC (SEQ ID NO:76)

D -- Cur2 1.38.1 light chain protein sequence

DIQMTQSPSSLSASVGDRVITICRASQGISNYLAWYQQKPGKVPNLLIYAASTLQ
SGVPSRFSGSGTDFSLTISSLQPEDVAAYYCQKCNSAPWTFGQGTTVEIK (SEQ
ID NO:34)



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FIGURE 14

A -- Cur2 1.39.1 heavy chain nucleotide sequence

GAGGTGCAGCTGGTGCAGTCGGGAACAGAGGTGAAAAAGCCCGGGGAGTCT
CTGAAGATCTCCTGTAAGGGTTCTGGATACAGGTTTACCAGCTACTGGATCGG
CTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATCATCTAT
CCTGGTGA CTCTGATACCAGATACAGCCCGTCCTTCCAAGGCCAGGTCACCA
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA
GGCCTCGGACACCGCCATGTATTACTGTGCGAGACATGGATCGTATTACTATA
ATTCGGGGAGTTATTATAACGTCTTTGACTACTGGGGCCAGGGAACCCTGGTC
ACCGTCTCCTCAG (SEQ ID NO:77)

B -- Cur2 1.39.1 heavy chain protein sequence

EVQLVQSGTEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIYPG
DSDTRYSPSFQGGQVTISADKSISTAYLQWSSLKASDTAMYYCARHGSYYNNSGS
YYNVFDYWGQGT LVT VSS (SEQ ID NO:35)

C -- Cur2 1.39.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
TATCAGCAGAAACCAGGGAAAGCCCCCTAAGCGCCTGATCTATGCTGCATCCA
GTTTGCAAAGTGGGGTCCCATCAAGGTTTCAAGCGCAGTGGATCTGGGACAGA
ATTCATCTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT
GTCTACAGCATAATAGTTACCCGTGGACGTTTCGGCCAAGGGACCAAGGTGGA
AATCAAAC (SEQ ID NO:78)

D -- Cur2 1.39.1 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ
SGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPWTFGQGTKVEIK (SEQ
ID NO:36)



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FIGURE 15

A -- Cur2 1.40.1 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGCAGTCGGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA
GTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCACTTATGATATCAA
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATGAA
CCCTAACAGTGGTAACACAGGCTATGCACAGAAGTTCCAGGGCAGAGTCACC
ATGACCAGGAACACCTCCCTAAGCACAGCCTACATGGAGCTGAGCAGCCTGA
GATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATATTGTAGTGGTGGT
AGCTGCTACCAACTACTACAACGGTATGGACGTCTGGGGCCAAGGGACCACG
GTCACCGTCTCCTCAG (SEQ ID NO:79)

B -- Cur2 1.40.1 heavy chain protein sequence

QVQLVQSGAEVKKPGASVKVSCKASGYTFTTYDINWVRQATGQGLEWMGWM
NPNSGNTGYAQKFQGRVTMTRNTSLSTAYMELSSLRSEDVAVYYCARDIVVVV
AATNYNGMDVWGQGTTVTVSS (SEQ ID NO:37)



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FIGURE 16

A -- Cur2 1.45 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGCAGTCGGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA
GTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAGTTATGATATCAA
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATGAA
CCCTAACAGTGGTAACACAGGCTATGCACAGAAGTTCCAGGGCAGAGTCACC
ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA
GATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGGCAGTGGATACAGCTA
TGGTTACGACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTC
ACCGTCTCCTCAG (SEQ ID NO:80)

B -- Cur2 1.45 heavy chain protein sequence

QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWM
NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDVAVYYCARGSGYSYG
YDYYYGMDVWGQGTITVTVSS (SEQ ID NO:38)

C -- Cur2 1.45 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCAATTGCCGGGCGAGTCAGGGCATTAGCAATGATTTAGCCTGG
TATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCA
CTTTGCAATTAGGGGTCCCATCTCGGTTCAAGTGGCAGTGGATCTGGGACAGAT
TTCATCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTG
TCAAAAGTATAACAGTGCCCCATTCACTTTCGGCCCTGGGACCAAAGTGGAT
ATCAAAC (SEQ ID NO:81)

D -- Cur2 1.45 light chain protein sequence

DIQMTQSPSSLSASVGDRVTINCRASQGISNDLAWYQQKPGKVPKLLIYAASLTQ
LGVPSRFSGSGSGTDFLTISLQPEDVATYYCQKYNAPFTFGPGTKVDIK (SEQ
ID NO:39)



FIGURE 17

A -- Cur2 1.46.1 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGCAGTCGGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA
GTGAAGGTCTCCTGCAAGGCTTCTGGATACTCCTTCACCAGTTATGATATCAA
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATGAA
CCCTAACAATGGTAACACAGGCTATGCACAGAAGTTCAGGGCAGAGTCACC
ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA
GATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATATTGTAGTGGTGGT
AACTGCTACGGACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACG
GTCACCGTCTCCTCAG (SEQ ID NO:82)

B -- Cur2 1.46.1 heavy chain protein sequence

QVQLVQSGAEVKKPGASVKVSCKASGYSFTSYDINWVRQATGQGLEWMGWM
NPNNGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDVAVYYCARDIVVVVT
ATDYYYGMDVWGQGTITVTVSS (SEQ ID NO:40)

C -- Cur2 1.46.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGG
TATCAGCAGAAACCAGGGAAAGCCCCCTAAGCGCCTGATTTTTGCTGCATCCA
GTTTGCCAAGTGGGGTCCCATCAAGGTTCAAGCGGAGTGGATCTGGGACAGA
ATTCATCTCACAAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACT
GTCTACAGCATAGTGGTTACCCTCCGACGTTCCGGCCAAGGGACCAAGGTGGA
AATCAAAC (SEQ ID NO:83)

D -- Cur2 1.46.1 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIFAASSLPS
GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHSGYPPTFGQGTKVEIK (SEQ ID
NO:41)



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FIGURE 18

A -- Cur2 1.48.1 heavy chain nucleotide sequence

CAGGTTTCAGCTGGTGCAGTCGGGAGCTGAGGTGAAGAAGCCTGGGGCCTCAG
TGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTTACCAGCTATGGTATCAGC
TGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCAGCG
CTTACAATGGTAACACAACTATGCACAGAAGCTCCAGGGCAGAGTCACCAT
GACCACAGACACATCCACGAGCACAGCCTACATGGAGCTGAGGAGCCTGAG
ATCTGACGACACGGCCGTGTATTACTGTGCGAGAGATGTTGAATATTACTATG
ATGGTAGTGGTTATTACTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACC
GTCTCCTCAG (SEQ ID NO:84)

B -- Cur2 1.48.1 heavy chain protein sequence

QVQLVQSGAEVKKPGASVKVSKASGYTFTSYGISWVRQAPGQGLEWMGWISA
YNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDVEYYD
GSGYYYFDYWGQGLTVTVSS (SEQ ID NO:42)

C -- Cur2 1.48.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGG
TATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCA
TTTTGCAAAGTGGGGTCCCATCAAGGTTCAAGCGGCAGTGGATCTGGGACAGA
TTTCACTCTCACCATCAGCAGCCTGCAGCCTGAGGATTTTGCATCTTACTATT
GTCAACAGTCTAACAGTTTCCCTCGGACGTTTCGGCCAAGGGACCAAGGTGGA
GATCAAAC (SEQ ID NO:85)

D -- Cur2 1.48.1 light chain protein sequence

DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQKPGKAPKLLIYAASILQ
SGVPSRFSGSGSGTDFLTISLQPEDFASYCQQSNSFPRTFGQGTKVEIK (SEQ
ID NO:43)



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FIGURE 19

A -- Cur2 1.49.1 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGCAGTCGGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA
GTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAGTTATGATATCAA
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATGAA
CCCTAACAGTGGTGACACAGGCTATGCACAGAAGTTCAGGGCAGAGTCACC
ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA
GATCTGAGGACACGGCCGTGTATTTCTGTGCGAGAATGAGGGATATAGTGGC
TACGAGCTATTACTACTACTTCTACGGTATGGACGTCTGGGGCCAAGGGACC
ACGGTCACCGTCTCCTCAG (SEQ ID NO:86)

B -- Cur2 1.49.1 heavy chain protein sequence

QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWM
NPNSGDTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDNAVYFCARMRDIVAT
SYYYFYGMVWVGQGTTVTVSS (SEQ ID NO:44)

C -- Cur2 1.49.1 light chain nucleotide sequence

GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCCGTCACCCCTGGAGAGCC
GGCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACA
ACTATTTGGATTGGTACCTGCTGAAGCCAGGGCAGTCTCCACAGCTCCTGATC
TATTTGGGTTCTAGTCGGGCCTCCGGGGTCCCTGACAGGTTTCAAGTGGCAGTGG
ATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATGTT
GGGGTTTATTACTGCATGCAAACCTCTACAACTATCACCTTCGGCCAAGGGA
CACGACTGGAGATTAAAC (SEQ ID NO:87)

D -- Cur2 1.49.1 light chain protein sequence

DIVMTQSPLSLPVTPGEPASISCRSSQSLHLSNGYNYLDWYLLKPGQSPQLLIYLG
SSRASGVPRFSGSGSDFTLKISRVEAEDVGVYYCMQTLQTITFGQGRLEIK
(SEQ ID NO:45)



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FIGURE 20

A -- Cur2 1.51 heavy chain nucleotide sequence

GAGGTGCAGCTGGTGCAGTCGGGAGCTGAGGTGAAAAAGCCCCGGGGAGTCT
CTGAAGATCTCCTGTAAGGGTTCTGGATACAGCTTTACCAGCTACTGGATCGG
CTGGGTGCGCCAGATGCCCGGGAAGGCCTGGAGTGGATGGGGATCATCTAT
CCTGGTGA CTCTGATGCCAAATACAGCCCGTCCTTCCAAGGCCAGGTCACCA
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA
GGCCTCGGACACCGCCATGTATTACTGTGCGAGACACTATGATTACGTTTGA
GGAATTATCGGTATACAGGGTGGTTCGACCCCTGGGGCCAGGGAACCCTGGT
CACCGTCTCCTCAG (SEQ ID NO:88)

B -- Cur2 1.51.1 heavy chain protein sequence

EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIYPG
DSDAKYSPSFQGGQVTISADKSISTAYLQWSSLKASDTAMYYCARHYDYVWRNY
RYTGWFDPWGQGTLVTVSS (SEQ ID NO:46)

C -- Cur2 1.51.1 light chain nucleotide sequence

GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAG
AGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCC
TGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCAT
CCAACAGGGCCACTGGCATCCCAGACAGGTTTCAGTGGCAGTGGGTCTGGGAC
AGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATT
ACTGTCAGCAGTATGGTAGCTCACTATTCACTTTCGGCCCTGGGACCAAAGTG
GATATCAAAC (SEQ ID NO:89)

D -- Cur2 1.51.1 light chain protein sequence

EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASNRA
TGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSLFTFGPGTKVDIK (SEQ
ID NO:47)



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FIGURE 21

A -- Cur2 6.4 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAG
TGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAGTTATGATATCAAC
TGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATAAAC
CCTAATAGTGGTAACACAGACTATGCACAGAAGTTCCAGGGCAGAGTCACCA
TGACCAGGGACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGAG
ATCTGAGGACACGGCCATATATTATTGTGTGAGAGGCTTTGGATACAGCTAT
AATTACGACTACTATTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCA
CCGTCTCCTCAGT (SEQ ID NO:90)

B -- Cur2 6.4 heavy chain amino acid sequence

QVQLVQSGAEVKKPGASVKVSCASGYTFTSYDINWVRQATGQGLEWMGWIN
PNSGNTDYAQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNY
DYYYGMDVWGQGTITVTVSS (SEQ ID NO:48)

C -- Cur2 6.4 light chain nucleotide sequence

GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAG
AGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGTAGTAGTTACTTAGCCT
GGTACCAGCAGAAGCCTGGCCAGGCTCCCAGGCTCCTCATCTATGCTACATC
CAGCAGGGCCACTGGCATCCCAGACAGGTTTCAGTGGCAGTGGGTCTGGGACA
GACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTA
CTGTCAGCAGTATGGTAGTTCACCGTGCAGTTTGGCCAGGGGACCAAGCTG
GAAATCAAGC (SEQ ID NO:91)

D -- Cur2 6.4 light chain amino acid sequence

EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRA
TGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFQGQGTKLEIK (SEQ
ID NO:49)



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FIGURE 22A

Clone	Germline genes used				No. of Nucleotide/ Amino acid changes						
					FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
CR2		V	D	J	V					D & J	
1.19.1	VH	V1-8	D3-16	JH6B	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK2	0/0	0/0	0/0	0/0	1/1	1/1	0/0
6.4.1	VH	V1-8	D5-18	JH6B	0/0	0/0	0/0	3/2	5/3	0/0	0/0
	VK	A27		JK2	0/0	3/0	1/0	2/2	0/0	1/0	0/0
1.18	VH	V1-8	D6-19	JH6B	1/0	0/0	0/0	1/0	0/0	0/0	0/0
	VK	A30		JK3	0/0	0/0	0/0	0/0	1/1	0/0	0/0
1.40.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0	0/0
	VK	mix									
1.45	VH	V1-8	DK4	JH6B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK3	1/1	1/1	0/0	1/1	0/0	0/0	0/0
1.46.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0	0/0
	VK	A30		JK1	0/0	0/0	2/1	1/1	0/0	2/2	0/0
1.49.1	VH	V1-8	D5-12	JH6B	1/0	0/0	0/0	1/1	1/1	0/0	0/0
	VK	A19		JK5	0/0	0/0	1/1	1/1	0/0	1/1	0/0
1.33	VH	V1-18	D21-9	JH6B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK4	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.48.1	VH	V1-18	D21-9	JH4B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	L5		JK1	0/0	0/0	0/0	1/1	2/1	1/1	0/0
1.6.1	VH	V3-21	D3-16	JH4B	0/0	4/4	0/0	1/1	1/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	1/1	0/0	0/0	0/0	0/0
1.17.1	VH	V3-33	D5-18	JH6B	2/1	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.24.1	VH	V3-33	D5-18	JH6B	0/0	2/1	0/0	1/1	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	1/0	0/0	0/0
1.38.1	VH	V3-33	D21-9	JH6B	1/0	0/0	0/0	3/3	2/1	0/0	0/0
	VK	A20		JK1	0/0	0/0	1/1	0/0	2/2	1/1	0/0
1.11.1	VH	V3-53	D4-17	JH6B	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A19		JK4	0/0	1/1	0/0	0/0	0/0	0/0	0/0
1.23.1	VH	V5-51	D3-10	JH4B	1/1	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	1/1	1/1	0/0	0/0	0/0
1.25.1	VH	V5-51	D3-10	JH4B	1/0	1/1	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.29	VH	V5-51	D5-12	JH6B	1/0	0/0	0/0	0/0	1/1	0/0	0/0
	VK	A19		JK2	0/0	0/0	1/0	0/0	1/1	0/0	0/0
1.39.1	VH	V5-51	D3-10	JH4B	2/1	1/1	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.51.1	VH	5-51	D3-16	JH5B	2/0	0/0	0/0	1/1	1/1	0/0	0/0
	VK	A27		JK3	0/0	0/0	0/0	1/1	0/0	0/0	0/0



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FIGURE 22B

Clone	Germline genes used				No. of Nucleotide/ Amino acid changes						
					FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
CR2		V	D	J	V					D & J	
1.40.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0	0/0
	VK	mix									
1.48.1	VH	V1-18	D21-9	JH4B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	L5		JK1	0/0	0/0	0/0	1/1	2/1	1/1	0/0
1.49.1	VH	V1-8	D5-12	JH6B	1/0	0/0	0/0	1/1	1/1	0/0	0/0
	VK	A19		JK5	0/0	0/0	1/1	1/1	0/0	1/1	0/0
1.11.1	VH	V3-53	D4-17	JH6B	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A19		JK4	0/0	1/1	0/0	0/0	0/0	0/0	0/0
1.29	VH	V5-51	D5-12	JH6B	1/0	0/0	0/0	0/0	1/1	0/0	0/0
	VK	A19		JK2	0/0	0/0	1/0	0/0	1/1	0/0	0/0
1.45	VH	V1-8	DK4	JH6B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK3	1/1	1/1	0/0	1/1	0/0	0/0	0/0
1.33	VH	V1-18	D21-9	JH6B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK4	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.38.1	VH	V3-33	D21-9	JH6B	1/0	0/0	0/0	3/3	2/1	0/0	0/0
	VK	A20		JK1	0/0	0/0	1/1	0/0	2/2	1/1	0/0
6.4.1	VH	V1-8	D5-18	JH6B	0/0	0/0	0/0	3/2	5/3	0/0	0/0
	VK	A27		JK2	0/0	3/0	1/0	2/2	0/0	1/0	0/0
1.51.1	VH	5-51	D3-16	JH5B	2/0	0/0	0/0	1/1	1/1	0/0	0/0
	VK	A27		JK3	0/0	0/0	0/0	1/1	0/0	0/0	0/0
1.19.1	VH	V1-8	D3-16	JH6B	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK2	0/0	0/0	0/0	0/0	1/1	1/1	0/0
1.18	VH	V1-8	D6-19	JH6B	1/0	0/0	0/0	1/0	0/0	0/0	0/0
	VK	A30		JK3	0/0	0/0	0/0	0/0	1/1	0/0	0/0
1.6.1	VH	V3-21	D3-16	JH4B	0/0	4/4	0/0	1/1	1/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	1/1	0/0	0/0	0/0	0/0
1.23.1	VH	V5-51	D3-10	JH4B	1/1	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	1/1	1/1	0/0	0/0	0/0
1.25.1	VH	V5-51	D3-10	JH4B	1/0	1/1	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.39.1	VH	V5-51	D3-10	JH4B	2/1	1/1	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.17.1	VH	V3-33	D5-18	JH6B	2/1	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.24.1	VH	V3-33	D5-18	JH6B	0/0	2/1	0/0	1/1	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	1/0	0/0	0/0
1.46.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0	0/0
	VK	A30		JK1	0/0	0/0	2/1	1/1	0/0	2/2	0/0



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FIGURE 23**Figure 23A**

										Section 1
	(1)	1	10	20	30	40	51			
CUR2-1.6.1_HC	(1)	EVQLVESGGGLVQPKGGSLRLSCAASGFTNFR								YNMNVROAPGKGLEWVSSI
VH3-21	(1)	EVQLVESGGGLVQPKGGSLRLSCAASGFTFS								YSMNVROAPGKGLEWVSSI
Consensus	(1)	EVQLVESGGGLVQPKGGSLRLSCAASGF								F SY MNWVRQAPGKGLEWSSI
										Section 2
	(52)	52	60	70	80	90	102			
CUR2-1.6.1_HC	(52)	SSSSSNIIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYTCARDIMI								
VH3-21	(52)	SSSSSVIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR----								
Consensus	(52)	SSSSS IYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR								
										Section 3
	(103)	103	110	126						
CUR2-1.6.1_HC	(103)	TFGGIIASFYFDYWGGTLVTVSS								
VH3-21	(99)	-----								
Consensus (103)										

Figure 23B

								Section 1	
	(1)	1	10	20	30	40	51		
CUR2-1.6.1_LC	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIKNDLGV					QOKPGKAPKRLIYAA		
A30	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIKNDLGV					QOKPGKAPKRLIYAA		
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIKNDLGV					QOKPGKAPKRLIYAA		
								Section 2	
	(52)	52	60	70	80	90	102		
CUR2-1.6.1_LC	(52)	SSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPLTFGGGT							
A30	(52)	SSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYP-----							
Consensus	(52)	SSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYP							
								Section 3	
	(103)	103	107						
CUR2-1.6.1_LC	(103)	KVEIK							
A30	(96)	-----							
Consensus	(103)								

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FIGURE 24**Figure 24A**

		Section 1					
		(1)	1	10	20	30	40 51
Cur2-1.11.1 HC	(1)	EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVI					
VH3-53	(1)	EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVI					
Consensus	(1)	EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVI					
		Section 2					
		(52)	52	60	70	80	90 102
Cur2-1.11.1 HC	(52)	YSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAGTVTTN					
VH3-53	(52)	YSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR-----					
Consensus	(52)	YSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCA					
		Section 3					
		(103)	103	110	120		
Cur2-1.11.1_HC	(103)	YYGMDVWGQGTTVTVSS					
VH3-53	(98)	-----					
Consensus	(103)						

Figure 24B

		Section 1					
		(1)	1	10	20	30	40 51
CUR2-1.11.1 LC	(1)	DIVMTQSPLSLPVTPGEPASISCRSSQSLLQSN GYN YLDWYLQKPGQSPQL					
A19	(1)	DIVMTQSPLSLPVTPGEPASISCRSSQSLLH SGN YN YLDWYLQKPGQSPQL					
Consensus	(1)	DIVMTQSPLSLPVTPGEPASISCRSSQSLL SGN YN YLDWYLQKPGQSPQL					
		Section 2					
		(52)	52	60	70	80	90 102
CUR2-1.11.1 LC	(52)	LIYLGSNRASGVEDRFSGSGSGTDFTLKI SRVEAEDVG VYYCMQALQTLP					
A19	(52)	LIYLGSNRASGVEDRFSGSGSGTDFTLKI SRVEAEDVG VYYCMQALQTP--					
Consensus	(52)	LIYLGSNRASGVEDRFSGSGSGTDFTLKI SRVEAEDVG VYYCMQALQT					
		Section 3					
		(103)	103	111			
CUR2-1.11.1 LC	(103)	GGGTRVEIK					
A19	(101)	-----					
Consensus	(103)						



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FIGURE 25**Figure 25A**

							Section 1
	(1)	1	10	20	30	40	51
CR2-1.17.1 HC	(1)	QVQLVESGGGVVQPG SL RLSCAASGFTFSSYGMHWVROAPGKGLEWVAVI					
VH3-33	(1)	QVQLVESGGGVVQPG SL RLSCAASGFTFSSYGMHWVROAPGKGLEWVAVI					
Consensus	(1)	QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMHWVROAPGKGLEWVAVI					
							Section 2
	(52)	52	60	70	80	90	102
CR2-1.17.1 HC	(52)	WYDGSNKYYADSVKGRFTISRDN SKNT LYLQMN SLRAED TA VYYC ARDQGY					
VH3-33	(52)	WYDGSNKYYADSVKGRFTISRDN SKNT LYLQMN SLRAED TA VYYC AR----					
Consensus	(52)	WYDGSNKYYADSVKGRFTISRDN SKNT LYLQMN SLRAED TA VYYC AR					
							Section 3
	(103)	103	110	126			
CR2-1.17.1 HC	(103)	RYAGYYYDYGMDVWGQGT TVTVSS					
VH3-33	(99)	-----					
Consensus	(103)						

Figure 25B

							Section 1
	(1)	1	10	20	30	40	52
CR2-1.17.1 LC	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQKPGKAPKRLIYAAS					
A30	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQKPGKAPKRLIYAAS					
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQKPGKAPKRLIYAAS					
							Section 2
	(53)	53	60	70	80	90	104
CR2-1.17.1 LC	(53)	SLQSGVPSRFSGSGSGTEFTLTISSLQPEDPATYYCLQHN SYPLTPGGG TKV					
A30	(53)	SLQSGVPSRFSGSGSGTEFTLTISSLQPEDPATYYCLQHN SYPLTPGGG TKV					
Consensus	(53)	SLQSGVPSRFSGSGSGTEFTLTISSLQPEDPATYYCLQHN SYPLTPGGG TKV					
							Section 3
	(105)	1067					
CR2-1.17.1 LC	(105)	EIK					
A30	(96)	---					
Consensus	(105)						



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FIGURE 26**Figure 26A**

						Section 1
						(1) 1 10 20 30 40 52
CR2-1.18_HC	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN				
VH1-8	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN				
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN				
						Section 2
						(53) 53 60 70 80 90 104
CR2-1.18_HC	(53)	PNSGNTGYAQKFGQGRVTMTNTSISTAYMELSSLRSEDTAVYYCAEREGIAVA				
VH1-8	(53)	PNSGNTGYAQKFGQGRVTMTNTSISTAYMELSSLRSEDTAVYYCAE-----				
Consensus	(53)	PNSGNTGYAQKFGQGRVTMTNTSISTAYMELSSLRSEDTAVYYCAR				
						Section 3
						(105) 105 110 126
CR2-1.18_HC	(105)	GTYYYYYYGMDVWGQGTTVTVSS				
VH1-8	(99)	-----				
Consensus	(105)					

Figure 26B

						Section 1	
	(1)	1	10	20	30	40	53
CR2-1.18_LC	(1)	DIQMTQSPFSSLSASVGDRVTITCRASQGIKNDLGWYQOKPKGKAPKRLIYAASS					
A30	(1)	DIQMTQSPFSSLSASVGDRVTITCRASQGIKNDLGWYQOKPKGKAPKRLIYAASS					
Consensus	(1)	DIQMTQSPFSSLSASVGDRVTITCRASQGIKNDLGWYQOKPKGKAPKRLIYAASS					
						Section 2	
	(54)	54	60	70	80	90	106
CR2-1.18_LC	(54)	LQSGVPFRFSGSGSGTEFTLTITSSLPEDFATYVCLQHNSTPFTPGPGTKVDI					
A30	(54)	LQSGVPFRFSGSGSGTEFTLTITSSLPEDFATYVCLQHNSTP-----					
Consensus	(54)	LQSGVPFRFSGSGSGTEFTLTITSSLPEDFATYVCLQHNSTP					
						Section 3	
	(107)	107					
CR2-1.18_LC	(107)	K					
A30	(96)	-					
Consensus	(107)						



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FIGURE 28**Figure 28A**

						Section 1
	(1)	1	10	20	30	40 51
Cur2-1.23.1_HC	(1)	EVQLVQBGAEVKKRPGESLKISC EGSYSPFTSYWIGWVRQMPGKGLEWMGII				
VH5-51	(1)	EVQLVQSGAEVKKRPGESLKI SC KSGSYSPFTSYWIGWVRQMPGKGLEWMGII				
Consensus	(1)	EVQLVQSGAEVKKRPGESLKISC GSGYSFTSYWIGWVRQMPGKGLEWMGII				
						Section 2
	(52)	52	60	70	80	90 102
Cur2-1.23.1_HC	(52)	YFGDSDFRYSESPFGQVTTISADKSI STAYLQWSSLKASDTAMYYCARHVS				
VH5-51	(52)	YFGDSDFRYSESPFGQVTTISADKSI STAYLQWSSLKASDTAMYYCAR----				
Consensus	(52)	YFGDSDFRYSESPFGQVTTISADKSI STAYLQWSSLKASDTAMYYCAR				
						Section 3
	(103)	103	110	126		
Cur2-1.23.1_HC	(103)	YYVSGSYYNVPDYWGQGLTVTVSS				
VH5-51	(99)	-----				
Consensus (103)						

Figure 28B

							Section 1
	(1)	1	10	20	30	40	51
Cur2-1.23.1_LC	(1)	DIQMTQSPSSLSASVGDRTITCRASQGIKNDLGWYQQIFGKAPKRLIYAA					
A30	(1)	DIQMTQSPSSLSASVGDRTITCRASQGIKNDLGWYQQKPGKAPKRLIYAA					
Consensus	(1)	DIQMTQSPSSLSASVGDRTITCRASQGIKNDLGWYQQ PGKAPKRLIYAA					
							Section 2
	(52)	52	60	70	80	90	102
Cur2-1.23.1_LC	(52)	SSLQRGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYPWTFGGGT					
A30	(52)	SSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYP-----					
Consensus	(52)	SSLQ GVPSPRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYP					
							Section 3
	(103)	103	107				
Cur2-1.23.1_LC	(103)	KVEIK					
A30	(96)	-----					
Consensus	(103)						



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FIGURE 29**Figure 29A**

								Section 1	
	(1)	1	10	20	30	40	51		
CR2-1.24.1_HC	(1)	QVQLVESGGGVVQPGRSRLSCAASGPFSSYGMHWVROAPGKGLEWVADI							
VH3-33	(1)	QVQLVESGGGVVQPGRSRLSCAASGPFSSYGMHWVROAPGKGLEWVAVI							
Consensus	(1)	QVQLVESGGGVVQPGRSRLSCAASGFSFSSYGMHWVROAPGKGLEWVA I							
								Section 2	
	(52)	52	60	70	80	90	102		
CR2-1.24.1_HC	(52)	WYDGSNKYYADSVKGRFTISRDNBKNLTLYLQMNSLRAEDTAVYYCARDQGY							
VH3-33	(52)	WYDGSNKYYADSVKGRFTISRDNBKNLTLYLQMNSLRAEDTAVYYCAR----							
Consensus	(52)	WYDGSNKYYADSVKGRFTISRDNBKNLTLYLQMNSLRAEDTAVYYCAR							
								Section 3	
	(103)	103	110	126					
CR2-1.24.1_HC	(103)	SYGYVYDYGMDVWGQGTTVTVSS							
VH3-33	(99)	-----							
Consensus	(103)								

Figure 29B

								Section 1
	(1)	1	10	20	30	40	52	
CR2-1.24.1 LC	(1)	DIQMTQSPESLSASVGDRVTITCRASQGIKNDLGWYQOKPGKAPKRLIYAAS						
A30	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIKNDLGWYQOKPGKAPKRLIYAAS						
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIKNDLGWYQOKPGKAPKRLIYAAS						
								Section 2
	(53)	53	60	70	80	90	104	
CR2-1.24.1 LC	(53)	SLQSGVPSRFSGSGSGTEFTLTISSLQPEDPATYYCLOHNSYEWTFGQGTKV						
A30	(53)	SLQSGVPSRFSGSGSGTEFTLTISSLQPEDPATYYCLOHNSYP-----						
Consensus	(53)	SLQSGVPSRFSGSGSGTEFTLTISSLQPEDPATYYCLOHNSYP						
								Section 3
	(105)	1067						
CR2-1.24.1 LC	(105)	EIK						
A30	(96)	---						
Consensus	(105)							



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FIGURE 30**Figure 30A**

Section 1							
	(1)	1	10	20	30	40	51
VH5-51	(1)	EVQLVQSGAEVKKRPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGII					
CR2-1.25.1_HC	(1)	EVQLVQSGAEVKKRPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGII					
Consensus	(1)	EVQLVQSGAEVKKRPGESLKISCKGSGY FTSYWIGWVRQMPGKGLEWMGII					
Section 2							
	(52)	52	60	70	80	90	102
VH5-51	(52)	YPGDSDDTRYSPSPFQSGQVTISADKSISTAYLQWSSLKASDTAMYYCAR----					
CR2-1.25.1_HC	(52)	YPGDSDDTRYSPSPFQSGQVTISADKSISTAYLQWSSLKASDTAMYYCARHGSI					
Consensus	(52)	YPGDSDDTRYSPSPFQSGQVTISADKSISTAYLQWSSLKASDTAMYYCAR					
Section 3							
	(103)	103	110	126			
VH5-51	(99)	-----					
CR2-1.25.1_HC	(103)	YYGSETYYNVFDYWGQGLTVTVSS					
Consensus	(103)						

Figure 30B

Section 1							
	(1)	1	10	20	30	40	52
A30	(1)	DIQMTQSPSSLSASVGDRTTITCRASQGIRNDLGWYQQRPGKAPKRLIYAAS					
CR2-1.25.1_LC	(1)	DIQMTQSPSSLSASVGDRTTITCRASQGIRNDLGWYQQRPGKAPKRLIYAAS					
Consensus	(1)	DIQMTQSPSSLSASVGDRTTITCRASQGIRNDLGWYQQRPGKAPKRLIYAAS					
Section 2							
	(53)	53	60	70	80	90	104
A30	(53)	SLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYP-----					
CR2-1.25.1_LC	(53)	SLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKV					
Consensus	(53)	SLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYP					
Section 3							
	(105)	1067					
A30	(96)	---					
CR2-1.25.1_LC	(105)	EIK					
Consensus	(105)						



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FIGURE 31**Figure 31A**

						Section 1
	(1)	1	10	20	30	40 52
VH5-51	(1)	EVQLVQSGAEVKKPGEISLKIISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIY				
CR2-1.29_HC	(1)	EVQLVQSGAEVKKPGEISLKIISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIY				
Consensus	(1)	EVQLVQSGAEVKKPGEISLKIISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIY				
						Section 2
	(53)	53	60	70	80	90 104
VH5-51	(53)	PGDSDDTRYSPSFQGGQTISADKSISTAYLQWSSILKASDTAMYYCAR-----				
CR2-1.29_HC	(53)	PGDSDDTRYSPSFQGGQTISADKSISTAYLQWSSILKASDTAMYYCARHVDVGA				
Consensus	(53)	PGDSDDTRYSPSFQGGQTISADKSISTAYLQWSSILKASDTAMYYCAR				
						Section 3
	(105)	105	110	129		
VH5-51	(99)	-----				
CR2-1.29_HC	(105)	TIGGGYYYYHGMDEVGQGTIVTVSS				
Consensus	(105)					

Figure 31B

		Section 1				
	(1)	1	10	20	30	40 53
A19	(1)	DIVMTQSPFLSLPVTPEGPASISCRSSQSLHNGYNYLDWYLQKPGQSPQLLI				
CR2-1.29_LC	(1)	DIVMTQSPFLSLPVTPEGPASISCRSSQSLHNGYNYLDWYLQKPGQSPQLLI				
Consensus	(1)	DIVMTQSPFLSLPVTPEGPASISCRSSQSLHNGYNYLDWYLQKPGQSPQLLI				
		Section 2				
	(54)	54	60	70	80	90 106
A19	(54)	YLGSNRAAGVPDRFSGSGSGTDFTLKISRVEAIDVGVYYCMQALQSP-----				
CR2-1.29_LC	(54)	YLGSNRAAGVPDRFSGSGSGTDFTLKISRVEAIDVGVYYCMQALQLMCSFGQ				
Consensus	(54)	YLGSNRAAGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQS				
		Section 3				
	(107)	107	113			
A19	(101)	-----				
CR2-1.29_LC	(107)	GTKLEIK				
Consensus	(107)					



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FIGURE 32

Figure 32A

Section 1					
	(1)	10	20	30	40
VH1-18	(1)	QVQLVQSGAEVRRPGASVKVSCRASGYTFTSYGTSWVRQAPGQGLEWMGWIS			52
CR2-1.33_HC	(1)	QVQLVQSGAEVKKPGASVKVSCRASGYTFTSYGISWVRQAPGQGLEWMGWIS			
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCRASGYTFTSYGISWVRQAPGQGLEWMGWIS			
Section 2					
	(53)	60	70	80	90
VH1-18	(53)	AYNGNTNYAQKLOGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR-----			104
CR2-1.33_HC	(53)	AYNGNTNYAQKLOGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDHYIDS			
Consensus	(53)	AYNGNTNYAQKLOGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR			
Section 3					
	(105)	110	127		
VH1-18 (99)	-----				
CR2-1.33_HC (105)	SDYLYYYXGLDVGQGTTVTVSS				
Consensus (105)					

Figure 32B

Section 1					
	(1)	10	20	30	40
A20	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQRPGKVPKLLIYAAS			53
CR2-1.33_LC	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQRPGKVPKLLIYAAS			
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQRPGKVPKLLIYAAS			
Section 2					
	(54)	60	70	80	90
A20	(54)	LQSGVPSRFSGSGSGTDFTLTISISLOPEDVATYYCQKYNAP-----			106
CR2-1.33_LC	(54)	LQSGVPSRFSGSGSGTDFTLTISISLOPEDVATYYCQKYNAPALTFGGGTKEI			
Consensus	(54)	LQSGVPSRFSGSGSGTDFTLTISISLOPEDVATYYCQKYNAP			
Section 3					
	(107)	107			
A20 (96)	-				
CR2-1.33_LC (107)	K				
Consensus (107)					



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FIGURE 33

Figure 33A

		Section 1				
	(1)	1	10	20	30	40 51
VH3-33	(1)	QVQLVESGGGVVQPGASLRRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAII				
CR2-1.38.1_HC	(1)	QVQLVESGGGVVQPGASLRRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAII				
Consensus	(1)	QVQLVESGGGVVQPGASLRRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAII				
		Section 2				
	(52)	52	60	70	80	90 102
VH3-33	(52)	WYDGSNKKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR----				
CR2-1.38.1_HC	(52)	WYDGSNKKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGYY				
Consensus	(52)	WYDGSNKKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR				
		Section 3				
	(103)	103	110	127		
VH3-33	(99)	-----				
CR2-1.38.1_HC	(103)	DSSDYLYYYYGMDVWGQGTITVTVSS				
Consensus	(103)					

Figure 33B

							Section 1
	(1)	1	10	20	30	40	52
A20	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQRKPGKVPKLLIYAAS					
CR2-1.38.1_LC	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQRKPGKVENLLIYAAS					
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQRKPGKVP LLIYAAS					
							Section 2
	(53)	53	60	70	80	90	104
A20	(53)	TLQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQRYNSAP-----					
CR2-1.38.1_LC	(53)	TLQSGVPSRFSGSGSGTDFTLTISSLQPEDVAATYCCQKCNAPWTFGQGTIV					
Consensus	(53)	TLQSGVPSRFSGSGSGTDFTLTISSLQPEDVA YYCQK NSAP					
							Section 3
	(105)	1067					
A20	(96)	---					
CR2-1.38.1_LC	(105)	EIK					
Consensus	(105)						



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FIGURE 34**Figure 34A**

								Section 1	
	(1)	1	10	20	30	40	51		
VH5-51	(1)	EVQLVQSGAEVKKRPGESLKIISCKGSGYSFTSYWIGWVRMPGKGLEWMGII							
CR2-1.39.1_HC	(1)	EVQLVQSGTEVKKRPGESLKIISCKGSGYRFTSYWIGWVRMPGKGLEWMGII							
Consensus	(1)	EVQLVQSG EVKKRPGESLKIISCKGSGY FTSYWIGWVRMPGKGLEWMGII							
								Section 2	
	(52)	52	60	70	80	90	102		
VH5-51	(52)	YPGDS DTRYSPSPFGQVTTISADKSISTAYLQWSSLKASDTAMYYCAR----							
CR2-1.39.1_HC	(52)	YPGDS DTRYSPSPFGQVTTISADKSISTAYLQWSSLKASDTAMYYCARHGSY							
Consensus	(52)	YPGDS DTRYSPSPFGQVTTISADKSISTAYLQWSSLKASDTAMYYCAR							
								Section 3	
	(103)	103	110	126					
VH5-51	(99)	-----							
CR2-1.39.1_HC	(103)	YYN8G8YYNVFDYWGQGLTVTVSS							
Consensus	(103)								

Figure 34B

								Section 1
	(1)	1	10	20	30	40	52	
A30	(1)	DIQMTQSPSSSLASAVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAAS						
CR2-1.39.1_LC	(1)	DIQMTQSPSSSLASAVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAAS						
Consensus	(1)	DIQMTQSPSSSLASAVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAAS						
								Section 2
	(53)	53	60	70	80	90	104	
A30	(53)	SLQSGVPSRFSGSGSGTEFTLTISISLOPEDPATYYCLOHNSYP-----						
CR2-1.39.1_LC	(53)	SLQSGVPSRFSGSGSGTEFTLTISISLOPEDPATYYCLOHNSYPWTFGQGTKV						
Consensus	(53)	SLQSGVPSRFSGSGSGTEFTLTISISLOPEDPATYYCLOHNSYP						
								Section 3
	(105)	1067						
A30	(96)	---						
CR2-1.39.1_LC	(105)	EIK						
Consensus	(105)							



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FIGURE 35

Figure 35A

								Section 1
	(1)	1	10	20	30	40	52	
VH1-8	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN						
CR2-1.45_HC	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN						
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN						
								Section 2
	(53)	53	60	70	80	90	104	
VH1-8	(53)	PNSGNTGYAQKPGGRVTMTNRTSISTAYMELSSLRSEDTAVYYCAR-----						
CR2-1.45_HC	(53)	PNSGNTGYAQKPGGRVTMTNRTSISTAYMELSSLRSEDTAVYYCARGSGYSY						
Consensus	(53)	PNSGNTGYAQKPGGRVTMTNRTSISTAYMELSSLRSEDTAVYYCAR						
								Section 3
	(105)	105	110	125				
VH1-8	(99)	-----						
CR2-1.45_HC	(105)	GYDYYYGMDVWGQGTTVTVSS						
Consensus	(105)							

Figure 35B

							Section 1
	(1)	1	10	20	30	40	53
A20	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQOKPGKVPKLLIYAAS					
CR2-1.45_LC	(1)	DIQMTQSPSSLSASVGDRVTINCRASQGISNDLAWYQQKPGKVPKLLIYAAS					
Consensus	(1)	DIQMTQSPSSLSASVGDRVTI CRASQGISN LAWYQQKPGKVPKLLIYAAS					
							Section 2
	(54)	54	60	70	80	90	106
A20	(54)	LQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNBAP-----					
CR2-1.45_LC	(54)	LQLGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNBAPFTFGPGTKVDI					
Consensus	(54)	LQ GVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNBAP					
							Section 3
	(107)	107					
A20	(96)	-					
CR2-1.45_LC	(107)	K					
Consensus	(107)						



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FIGURE 36**Figure 36A**

							Section 1
	(1)	1	10	20	30	40	51
VH1-8	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYFTSYDINWVRQATGQGLEWMGWM					
CR2-1.46.1_HC	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYFTSYDINWVRQATGQGLEWMGWM					
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYFTSYDINWVRQATGQGLEWMGWM					
							Section 2
	(52)	52	60	70	80	90	102
VH1-8	(52)	NPNSGNTGYAQKFGGRVTMTNTSISTAYMELSSLRSEDVAVYYCAR----					
CR2-1.46.1_HC	(52)	NPNSGNTGYAQKFGGRVTMTNTSISTAYMELSSLRSEDVAVYYCARDIVV					
Consensus	(52)	NPN GNTGYAQKFGGRVTMTNTSISTAYMELSSLRSEDVAVYYCAR					
							Section 3
	(103)	103	110	126			
VH1-8	(99)	-----					
CR2-1.46.1_HC	(103)	VVTATDYYYGMDVWGQTTVTVSS					
Consensus	(103)						

Figure 36B

		Section 1				
	(1)	1	10	20	30	40 52
A30	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIKNDLGWYQKPKAPKRLTFAAS				
CR2-1.46.1_LC	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIKNDLGWYQKPKAPKRLTFAAS				
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIKNDLGWYQKPKAPKRLTFAAS				
		Section 2				
	(53)	53	60	70	80	90 104
A30	(53)	SLQSGVPSPRFGSGSGTEFTLTISSLQPEDFATYYCLQHNSYP-----				
CR2-1.46.1_LC	(53)	SLPESGVPSPRFGSGSGTEFTLTISSLQPEDFATYYCLQHSGYPPTFGQGTKV				
Consensus	(53)	SL SGVPSRFGSGSGTEFTLTISSLQPEDFATYYCLQH YP				
		Section 3				
	(105)	1087				
A30	(96)	---				
CR2-1.46.1_LC	(105)	EIK				
Consensus	(105)					



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FIGURE 37

Figure 37A

							Section 1
	(1)	1	10	20	30	40	51
CR2-1.48.1_HC	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGGQGLEWMGWI					
VH1-18	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGGQGLEWMGWI					
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGGQGLEWMGWI					
							Section 2
	(52)	52	60	70	80	90	102
CR2-1.48.1_HC	(52)	SAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDVEY					
VH1-18	(52)	SAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR---					
Consensus	(52)	SAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR					
							Section 3
	(103)	103	110	125			
CR2-1.48.1_HC	(103)	YYDGSGLYYFDYWGQGLTVTVSS					
VH1-18	(99)	-----					
Consensus	(103)						

Figure 37B

		Section 1				
	(1)	1	10	20	30	40 52
CR2-1.48.1_LC	(1)	DIQMTQSPSSVSASVGDRTTTCRASQGISSWLAHWYQKPKAPKLLIYAAS				
L5	(1)	DIQMTQSPSSVSASVGDRTTTCRASQGISSWLAHWYQKPKAPKLLIYAAS				
Consensus	(1)	DIQMTQSPSSVSASVGDRTTTCRASQGISSWLAHWYQKPKAPKLLIYAAS				
		Section 2				
	(53)	53	60	70	80	90 104
CR2-1.48.1_LC	(53)	ILQSGVPSRFSGSGSGTDFTLTISSLQPEDFAFYCQQNSFPRTFGQGTKV				
L5	(53)	SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFAFYCQQNSFP-----				
Consensus	(53)	LQSGVPSRFSGSGSGTDFTLTISSLQPEDFASYCQQANSFP				
		Section 3				
	(105)	1057				
CR2-1.48.1_LC	(105)	EIK				
L5	(96)	---				
Consensus	(105)					



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FIGURE 38

Figure 38A

		Section 1						
		(1)	1	10	20	30	40	51
CR2-1.49.1_HC	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVROATGQGLEWMGWM						
VH1-8	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVROATGQGLEWMGWM						
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVROATGQGLEWMGWM						
		Section 2						
		(52)	52	60	70	80	90	102
CR2-1.49.1_HC	(52)	NPNSGDTGYAQKPGGRVTMTNTSISTAYMELSSLRSEDTAVYFCARMRDI						
VH1-8	(52)	NPNSGNTGYAQKPGGRVTMTNTSISTAYMELSSLRSEDTAVYFCAR----						
Consensus	(52)	NPNSG TGYAQKPGGRVTMTNTSISTAYMELSSLRSEDTAVYFCAR						
		Section 3						
		(103)	103	110	127			
CR2-1.49.1_HC	(103)	VATSYYYYFYGMVDVWGQGTITVTVSS						
VH1-8	(99)	-----						
Consensus	(103)							

Figure 38B

										Section 1	
		(1)	1	10	20	30	40	52			
CR2-1.49.1_LC	(1)	DIVMTQBELSLLEVTEGEPASISCRSSQSLLHSGNGYNYLDWYLLKPGQSPQLL									
A19	(1)	DIVMTQBELSLPVTGPGEPAISCRSSQSLLHSGNGYNYLDWYLLKPGQSPQLL									
Consensus	(1)	DIVMTQSPSLSLPVTGPGEPAISCRSSQSLLHSGNGYNYLDWYLLKPGQSPQLL									
										Section 2	
		(53)	53	60	70	80	90	104			
CR2-1.49.1_LC	(53)	IYLGSSRASGVDPDRPSGSGSGTDLFTLKISRVEAEDVGVIYCMQTLQITITFGQ									
A19	(53)	IYLGSSNRASGVDPDRPSGSGSGTDLFTLKISRVEAEDVGVIYCMQALQTP----									
Consensus	(53)	IYLGSRASGVDPDRPSGSGSGTDLFTLKISRVEAEDVGVIYCMQLQT									
										Section 3	
		(105)	105	111							
CR2-1.49.1_LC	(105)	GTRLEIK									
A19	(101)	-----									
Consensus	(105)										



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FIGURE 39**Figure 39A**

		Section 1					
		(1) 1	10	20	30	40	51
CR2-1.51.1 HC	(1)	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRMPGKGLEWMGII					
VH5-51	(1)	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRMPGKGLEWMGII					
Consensus	(1)	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRMPGKGLEWMGII					
		Section 2					
		(52) 52	60	70	80	90	102
CR2-1.51.1 HC	(52)	YFGDSDA YSPSFQGQVTISADKSIISTAYLQWSSLKASDTAMYYCARHYDY					
VH5-51	(52)	YFGDSDT YSPSFQGQVTISADKSIISTAYLQWSSLKASDTAMYYCAR----					
Consensus	(52)	YFGDSD K YSPSFQGQVTISADKSIISTAYLQWSSLKASDTAMYYCAR					
		Section 3					
		(103) 103	110	126			
CR2-1.51.1_HC	(103)	VWRNYRYTGWFDPWGQGLTVTVSS					
VH5-51	(99)	-----					
Consensus	(103)						

Figure 39B

		Section 1					
		(1) 1	10	20	30	40	52
CR2-1.51.1 LC	(1)	EIVLTQSPGTLISLSPGERATLSCRABQSIVSSSYLAWYQOKPGQAPRLIIYGA					
A27	(1)	EIVLTQSPGTLISLSPGERATLSCRABQSIVSSSYLAWYQOKPGQAPRLIIYGA					
Consensus	(1)	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQOKPGQAPRLIIYGA					
		Section 2					
		(53) 53	60	70	80	90	104
CR2-1.51.1 LC	(53)	SNRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGSLLPTFGPGTK					
A27	(53)	SSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGSPP-----					
Consensus	(53)	S RATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGS					
		Section 3					
		(105) 10508					
CR2-1.51.1 LC	(105)	VDIK					
A27	(97)	----					
Consensus	(105)						



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FIGURE 40**Figure 40A**

								Section 1
	(1)	1	10	20	30	40	52	
Cur2-6.4.1 hc	(1)	QVQLVQSGAEVVRKEGASVKVSCKASGYTFTSYDINWVROATGQGLEWMGWIN						
VH1-8	(1)	QVQLVQSGAEVVRKEGASVKVSCKASGYTFTSYDINWVROATGQGLEWMGWIN						
Consensus	(1)	QVQLVQSGAEVVRKEGASVKVSCKASGYTFTSYDINWVROATGQGLEWMGWIN						
								Section 2
	(53)	53	60	70	80	90	104	
Cur2-6.4.1 hc	(53)	PNSGNTDYAQKFQGRVTMTRDTSTISTAYMELSSLRSEDTAIYYCVRGPGYSY						
VH1-8	(53)	PNSGNTGYAQKFQGRVTMTRNTSTISTAYMELSSLRSEDTAIYYCAR-----						
Consensus	(53)	PNSGNT YAQKFQGRVTMTR TSISTAYMELSSLRSEDTAIYYC R						
								Section 3
	(105)	105	110	125				
Cur2-6.4.1 hc	(105)	NYDYXXGMDVWGQGTITVTVSS						
VH1-8	(99)	-----						
Consensus	(105)							

Figure 40B

								Section 1
	(1)	1	10	20	30	40	52	
Cur2-6.4.1 Lc	(1)	EIVLTQSPGTL SL SPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLITYT						
A27	(1)	EIVLTQSPGTL SL SPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLITYA						
Consensus	(1)	EIVLTQSPGTL SL SPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLITYA						
								Section 2
	(53)	53	60	70	80	90	104	
Cur2-6.4.1 Lc	(53)	SSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SP FCSPFGQGTK						
A27	(53)	SSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SP -----						
Consensus	(53)	SSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SP						
								Section 3
	(105)	10908						
Cur2-6.4.1 Lc	(105)	LEIK						
A27	(97)	----						
Consensus	(105)							

Figure 41A

CLONE #	VH	#DE L	VH END	# N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH	# del	JH Segment
1.19.1	DP-15/1-8	-1	CGAGAG (SEQ ID NO:92)	3	ACG	D3-16	28	TTATGATTACGTTT GGGGAGTTATCGT (SEQ ID NO:93)	2	GC	JH6 B	-12	ACTACG (SEQ ID NO:94)
1.19.2	DP-15/1-8	-1	CGAGAG (SEQ ID NO:92)	3	ACG	D3-16	28	TTATGATTACGTTT GGGGAGTTATCGT (SEQ ID NO:93)	2	GC	JH6 B	-12	ACTACG (SEQ ID NO:94)
1.19.3	DP-15/1-8	-1	CGAGAG (SEQ ID NO:92)	3	ACG	D3-16	28	TTATGATTACGTTT GGGGAGTTATCGT (SEQ ID NO:93)	2	GC	JH6 B	-12	ACTACG (SEQ ID NO:94)
6.4.1	DP-15/1-8	0	GAGAGG (SEQ ID NO:95)	3	CTT	D5-18	12	TGATACAGCTA (SEQ ID NO:96)	2	TA	JH6 B	0	ATTACTAC (SEQ ID NO:97)
6.4.2	DP-15/1-8	0	GAGAGG (SEQ ID NO:95)	3	CTT	D5-18	12	TGATACAGCTA (SEQ ID NO:96)	2	TA	JH6 B	0	ATTACTAC (SEQ ID NO:97)
6.4.3	DP-15/1-8	0	GAGAGG (SEQ ID NO:95)	3	CTT	D5-18	12	TGATACAGCTA (SEQ ID NO:96)	2	TA	JH6 B	0	ATTACTAC (SEQ ID NO:97)

CLONE	vk	#de	vk end	#n	N SEQ	Jk	# del	JK end
-------	----	-----	--------	----	-------	----	-------	--------

1.19.1	A30	-3	TTACCC (SEQ ID NO:98)	6	GTGCAG (SEQ ID NO:99)	JK2	-7	TTTTGG (SEQ ID NO:100)
1.19.2	A30	-3	TTACCC (SEQ ID NO:98)	6	GTGCAG (SEQ ID NO:99)	JK2	-7	TTTTGG (SEQ ID NO:100)



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Figure 42A

CLONE #	VH	#DEL	VH END	# N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH	# del	JH Segment
1.6.1	DP-77/3-21	0	GAGAGA (SEQ ID NO:104)	0	0	D3-16	22	TATTATGATTAC GTTTGGGGGA (SEQ ID NO:105)	14	ATTATCGCC TCGTT (SEQ ID NO:106)	JH4B	-1	CTACTT (SEQ ID NO:107)
1.6.1	DP-77/3-21	0	GAGAGA (SEQ ID NO:104)	0	0	D3-16	22	TATTATGATTAC GTTTGGGGGA (SEQ ID NO:105)	14	ATTATCGCC TCGTT (SEQ ID NO:106)	JH4B	-1	CTACTT (SEQ ID NO:107)
1.6.1	DP-77/3-21	0	GAGAGA (SEQ ID NO:104)	0	0	D3-16	22	TATTATGATTAC GTTTGGGGGA (SEQ ID NO:105)	14	ATTATCGCC TCGTT (SEQ ID NO:106)	JH4B	-1	CTACTT (SEQ ID NO:107)
1.11.1	DP-42/3-53	-5	AGAGA (SEQ ID NO:108)	3	GGA	D4-17	10	ACGGTGACTA (SEQ ID NO:109)	5	GGAAT (SEQ ID NO:110)	JH6B	-2	TACTACT A (SEQ ID NO:111)
1.11.2	DP-42/3-53	-5	AGAGA (SEQ ID NO:108)	3	GGA	D4-17	10	ACGGTGACTA (SEQ ID NO:109)	5	GGAAT (SEQ ID NO:110)	JH6B	-2	TACTACT A (SEQ ID NO:111)
1.23.1	DP-73/5-51	0	GAGACA (SEQ ID NO:112)	18	TGTATCGTATTACT (SEQ ID NO:113)	D3-10	19	TTCGGGAGTTA TTATAAC (SEQ ID NO:114)	2	GT	JH4B	-4	CTTTGA (SEQ ID NO:115)
1.23.2	DP-73/5-51	0	GAGACA (SEQ ID NO:112)	18	TGTATCGTATTACT (SEQ ID NO:113)	D3-10	19	TTCGGGAGTTA TTATAAC (SEQ ID NO:114)	2	GT	JH4B	-4	CTTTGA (SEQ ID NO:115)
CLONE	Vk	#del	Vk end		N SEQ	Jk	# del	JK end					





				#n				
1.6.1	A30	-3	TTACCC (SEQ ID NO:116)	0	0	JK4	0	GCTCACT (SEQ ID NO:117)
1.6.2	A30	-3	TTACCC (SEQ ID NO:116)	0	0	JK4	0	GCTCACT (SEQ ID NO:117)
1.6.3	A30	-3	TTACCC (SEQ ID NO:116)	0	0	JK4	0	GCTCACT (SEQ ID NO:117)
1.11.1	A3/A19/DPK	-4	AAACTC (SEQ ID NO:118)	0	0	JK4	-2	TCACTTTC (SEQ ID NO:119)
1.11.2	A3/A19/DPK	-4	AAACTC (SEQ ID NO:118)	0	0	JK4	-2	TCACTTTC (SEQ ID NO:119)
1.23.1	A30	-3	TTACCC (SEQ ID NO:120)	0	0	JK1	0	GTGGAC (SEQ ID NO:120)
1.23.2	A30	-3	TTACCC (SEQ ID NO:120)	0	0	JK1	0	GTGGAC (SEQ ID NO:120)

Figure 42B

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Figure 43A

CLONE #	VH	#DEL	VH END	#N's	N Sequence	DH	Size of D	D Sequence	#N's	N Sequence	JH	#del	JH Segment
1.17.1	DP-50/3-33	0	GAGAGA (SEQ ID NO:121)	4	TCAA	D6-18	8	GGATACA (SEQ ID NO:122)	9	ATATGCTG G (SEQ ID NO:123)	JH6B	-1	TTACTACT (SEQ ID NO:124)
1.17.2	DP-50/3-33	0	GAGAGA (SEQ ID NO:121)	4	TCAA	D6-18	8	GGATACA (SEQ ID NO:122)	9	ATATGCTG G (SEQ ID NO:123)	JH6B	-1	TTACTACT (SEQ ID NO:124)
1.17.3	DP-50/3-33	0	GAGAGA (SEQ ID NO:121)	4	TCAA	D6-18	8	GGATACA (SEQ ID NO:122)	9	ATATGCTG G (SEQ ID NO:123)	JH6B	-1	TTACTACT (SEQ ID NO:124)
1.18	DP-15/1-8	1	CGAGAG (SEQ ID NO:125)	1	A	D6-19	19	GGGTATAG CAGTGGCT GG (SEQ ID NO:126)	4	GACA	JH6B	-2	TACTAC (SEQ ID NO:127)
1.24.1	DP-50/3-33	0	GAGAGA (SEQ ID NO:128)	4	TCAG	DK4	18	GGATACAG CTATGGTT AC (SEQ ID NO:129)	2	GT	JH6B	-4	CTACTA (SEQ ID NO:130)
1.24.2	DP-50/3-33	0	GAGAGA (SEQ ID NO:128)	4	TCAG	DK4	18	GGATACAG CTATGGTT AC (SEQ ID NO:129)	2	GT	JH6B	-4	CTACTA (SEQ ID NO:130)
1.25.1	DP-73/5-51	0	GAGACA (SEQ ID NO:131)	6	TGGATC (SEQ ID NO:132)	D3-10	30	GTATATTA TGGTTCGG AGACTTATT ATAA	3	TGT	JH4B	-4	CTTTGA (SEQ ID NO:135)

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Figure 43B

CLONE #	VH	#DEL	VH END	#N's	N Sequence	DH	Size of D	D Sequence	#N's	N Sequence	JH	#del	JH Segment
1.25.2	DP-73/5-51	0	GAGACA (SEQ ID NO:131)	6	TGGATC (SEQ ID NO:132)	D3-10	30	GTATATTA TGGTTCGG AGACTTATT ATAA (SEQ ID NO:133)	3	TGT	JH4B	-4	CTTTGA (SEQ ID NO:134)
1.28	DP-73/5-51	0	GAGACA (SEQ ID NO:135)	1	C	D5-12	21	GTGGATgT AGGGGCT ACGATT (SEQ ID NO:136)	7	GGGGAT (SEQ ID NO:137)	JH6B	0	ATTACTAC (SEQ ID NO:138)
1.33	DP-14/1-18	0	GAGAGA (SEQ ID NO:139)	2	TC	D21-9	18	ATTACTAT GATAGTAG TG (SEQ ID NO:140)	7	ATTATCT (SEQ ID NO:141)	JH6B	-4	CTACTA (SEQ ID NO:142)
1.38.1	DP-50/3-33	1	CGAGAG (SEQ ID NO:143)	2	GA	D21-9	19	TATTACTA TGATAGTA GTG (SEQ ID NO:144)	7	ATTATCT (SEQ ID NO:145)	JH6B	-4	CTACTA (SEQ ID NO:146)
1.38.1	DP-73/5-51	0	GAGACA (SEQ ID NO:147)	6	TGGATC (SEQ ID NO:148)	D3-10	31	GTATTACT ATaattCG GGGAGTTA TTATAAC (SEQ ID NO:149)	2	GT	JH4B	-4	CTTTGA (SEQ ID NO:150)
1.38.2	DP-73/5-51	0	GAGACA (SEQ ID NO:147)	6	TGGATC (SEQ ID NO:148)	D3-10	31	GTATTACT ATaattCG GGGAGTTA TTATAAC (SEQ ID NO:149)	2	GT	JH4B	-4	CTTTGA (SEQ ID NO:150)

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Figure 43C

CLONE #	VH	#DEL	VH END	#N's	N Sequence	DH	Size of D	D Sequence	#N's	N Sequence	JH	#del	JH Segment
1.40.1	DP-16/1-8	1	CGAGAG (SEQ ID NO:151)	0	0	D2	25	ATATTGTA GTGGTGGT AGCTGCTA C (SEQ ID NO:152)	2	CA	JH6B	-6	ACTACT (SEQ ID NO:153)
1.40.2	DP-16/1-8	1	CGAGAG (SEQ ID NO:151)	0	0	D2	25	ATATTGTA GTGGTGGT AGCTGCTA C (SEQ ID NO:152)	2	CA	JH6B	-6	ACTACT (SEQ ID NO:153)
1.45	DP-16/1-8	0	GAGAGG (SEQ ID NO:154)	2	CA	DK4	20	GTGGATAC AGCTATGG TTAC (SEQ ID NO:155)	1	G	JH6B	-6	ACTACT (SEQ ID NO:156)
1.46.1	DP-16/1-8	1	CGAGAG (SEQ ID NO:157)	0	0	D2	25	ATATTGTA GT GGTGGTA GCTGCTAC (SEQ ID NO:158)	2	GG	JH6B	-6	ACTACT (SEQ ID NO:159)
1.46.2	DP-16/1-8	1	CGAGAG (SEQ ID NO:157)	0	0	D2	25	ATATTGTA GTGGTGGT AGCTGCTA C (SEQ ID NO:158)	2	GG	JH6B	-6	ACTACT (SEQ ID NO:159)
1.46.1	DP-14/1-18	1	CGAGAG (SEQ ID NO:160)	7	TGTTGAA (SEQ ID NO:161)	D21-9	20	TATTACTA TGATgGTA GTGGTTAT (SEQ ID NO:162)	1	T	JH4B	0	ACTACT (SEQ ID NO:163)
1.46.2	DP-14/1-18	1	CGAGAG	7	TGTTGAA	D21-9	20	TATTACTA	1	T	JH4B	0	ACTACT

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Figure 43D

CLONE #	VH	#DEL	VH END (SEQ ID NO:160)	#N's	N Sequence (SEQ ID NO:161)	DH	Size of D	D Sequence (SEQ ID NO:162)	#N's	N Sequence	JH	#del	JH Segment (SEQ ID NO:163)
1.49.1	DP-15/1-8	2	GCGAGA (SEQ ID NO:164)	5	ATGAG (SEQ ID NO:165)	D5-12	17	GGATATAG A (SEQ ID NO:166)	3	GCT	JH6B	0	ATTACTAC (SEQ ID NO:167)
1.49.2	DP-15/1-8	2	GCGAGA (SEQ ID NO:164)	5	ATGAG (SEQ ID NO:165)	D5-12	17	GGATATAG A (SEQ ID NO:166)	3	GCT	JH6B	0	ATTACTAC (SEQ ID NO:167)
1.51.1	DP-73/5-51	0	GAGACA (SEQ ID NO:168)	1	C	D3-16	31	TATGATTA CGTTTGGa GGAATTAT CGGTATA (SEQ ID NO:169)	5	CAGGG (SEQ ID NO:170)	JH5B	-5	TGGTTC (SEQ ID NO:171)
1.51.2	DP-73/5-51	0	GAGACA (SEQ ID NO:168)	1	C	D3-16	31	TATGATTA CGTTTGGa GGAATTAT CGGTATA (SEQ ID NO:169)	5	CAGGG (SEQ ID NO:170)	JH5B	-5	TGGTTC (SEQ ID NO:171)

CLONE	vk	#del	vk end	#n	N SEQ	JK	#del	JK end
-------	----	------	--------	----	-------	----	------	--------

1.17.1	A30	3	TTACCC (SEQ ID NO:172)	0	0	JK4	0	GCTCACT (SEQ ID NO:173)
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Figure 43E

CLONE	Vk	#del	Vk end	#n	N SEQ	JK	# del	JK end
1.17.2	A30	3	TTACCC (SEQ ID NO:172)	0	0	JK4	0	GCTCACT (SEQ ID NO:173)
1.17.3	A30	3	TTACCC (SEQ ID NO:172)	0	0	JK4	0	GCTCACT (SEQ ID NO:173)
1.18	A30	3	TTACCC (SEQ ID NO:174)	0	0	JK3	0	ATTGAC (SEQ ID NO:175)
1.24.1	A30	3	TTACCC (SEQ ID NO:176)	0	0	JK1	0	GTGGAC (SEQ ID NO:177)
1.24.2	A30	3	TTACCC (SEQ ID NO:176)	0	0	JK1	0	GTGGAC (SEQ ID NO:177)
1.25.1	A30	3	TTACCC (SEQ ID NO:178)	0	0	JK1	0	GTGGAC (SEQ ID NO:179)
1.25.2	A30	3	TTACCC (SEQ ID NO:178)	0	0	JK1	0	GTGGAC (SEQ ID NO:179)
1.29	A3/A19/DPK	7	CTACAA (SEQ ID NO:180)	14	TCTCTCATG TGCAG (SEQ ID NO:181)	JK2	-7	TTTTGG (SEQ ID NO:182)
1.33	A20/DPK4	3	TGCCCC (SEQ ID NO:183)	0	0	JK4	0	GCTCAC (SEQ ID NO:184)
1.38.1	A20/DPK4	3	TGCCCC (SEQ ID NO:185)	0	0	JK1	0	GTGGAC (SEQ ID NO:186)
1.39.1	A30	3	TTACCC (SEQ ID NO:187)	0	0	JK1	0	GTGGAC (SEQ ID NO:188)

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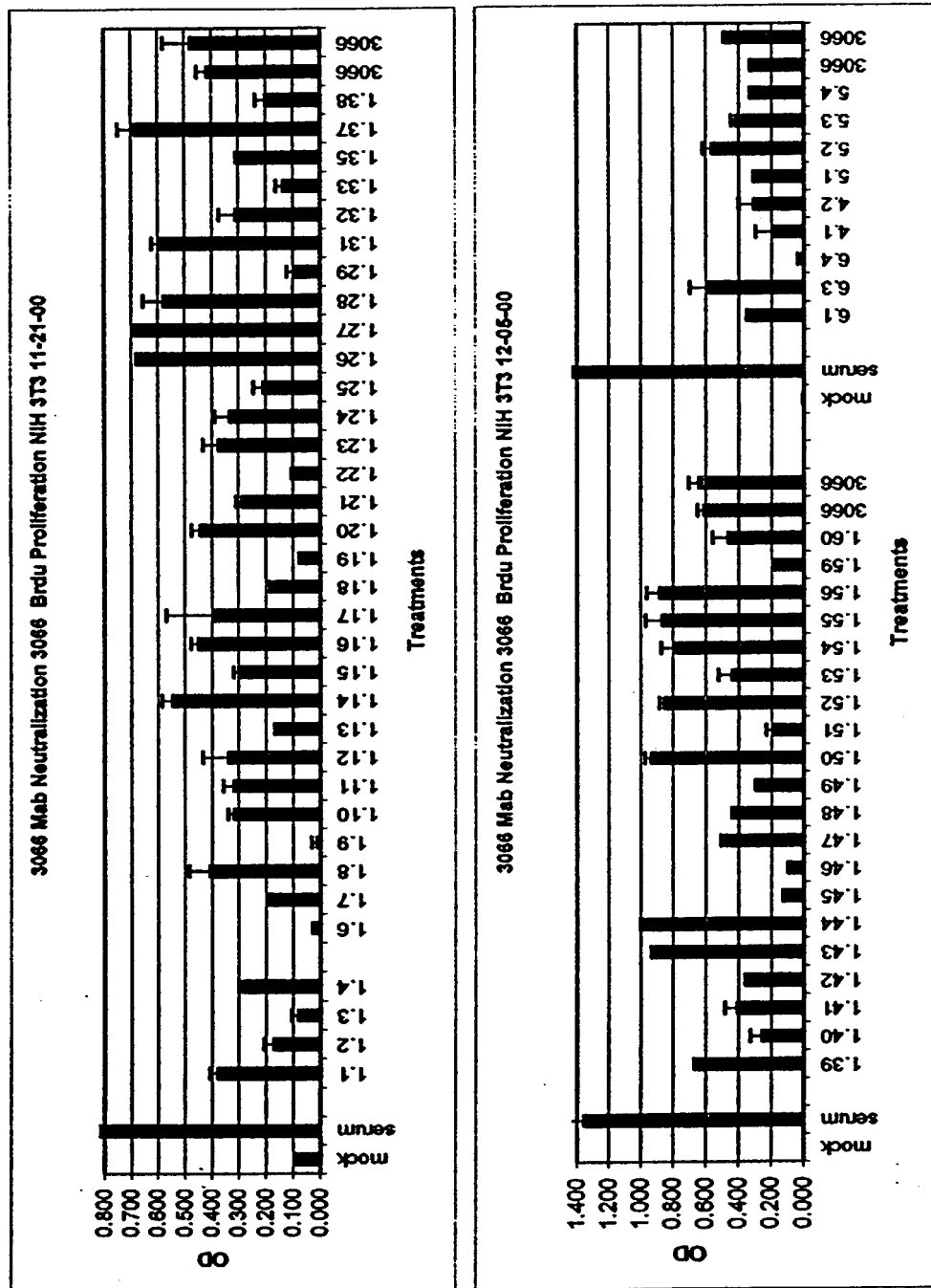
Figure 43F

CLONE	vk	#del	vk end	#n	N SEQ	JK	#del	JK end
1.39.2	A30	3	TTACCC (SEQ ID NO:187)	0	0	JK1	0	GTGGAC (SEQ ID NO:188)
1.45	A20/DPK4	3	TGCCCC (SEQ ID NO:189)	0	0	JK3	0	ATTCAC (SEQ ID NO:190)
1.46.1	A30	0	CCCTCC (SEQ ID NO:191)	0	0	JK1	-3	GACGTT (SEQ ID NO:192)
1.46.2	A30	0	CCCTCC (SEQ ID NO:191)	0	0	JK1	-3	GACGTT (SEQ ID NO:192)
1.48.1	L5/DPK5V	1	TCCCTC (SEQ ID NO:193)	0	0	JK1	-2	GGACGTT (SEQ ID NO:194)
1.48.2	L5/DPK5V	1	TCCCTC (SEQ ID NO:193)	0	0	JK1	-2	GGACGTT (SEQ ID NO:194)
1.49.1	A3/A19/DPK	5	CAAACT (SEQ ID NO:195)	0	0	JK5	-1	ATCACC (SEQ ID NO:196)
1.49.2	A3/A19/DPK	5	CAAACT (SEQ ID NO:195)	0	0	JK5	-1	ATCACC (SEQ ID NO:196)
1.51.1	A27/A27A	4	GCTCAC (SEQ ID NO:197)	1	T	JK3	0	ATTCAC (SEQ ID NO:198)
1.51.1	A27/A27A	4	GCTCAC (SEQ ID NO:197)	1	T	JK3	0	ATTCAC (SEQ ID NO:198)

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FIGURE 44



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FIGURE 45

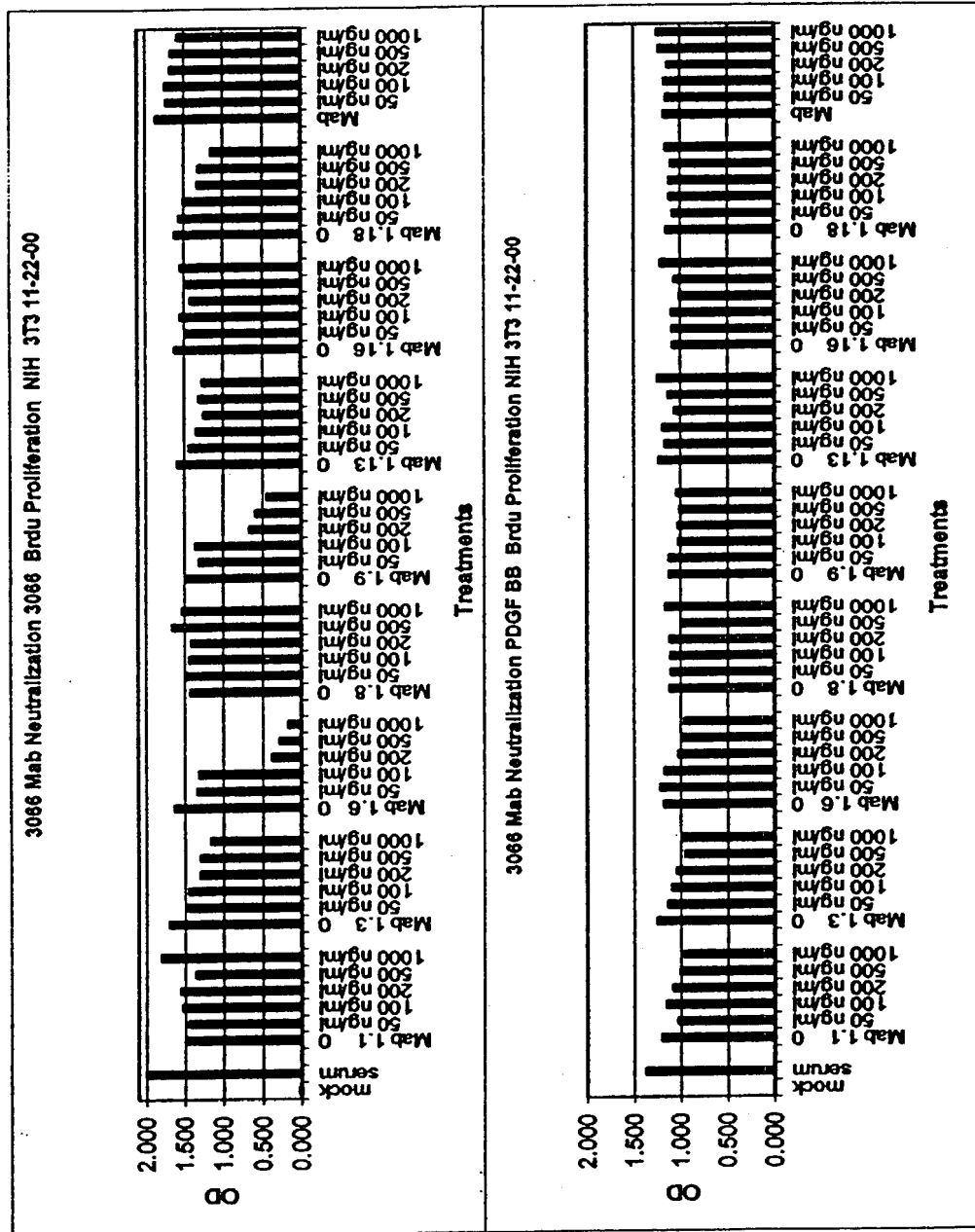
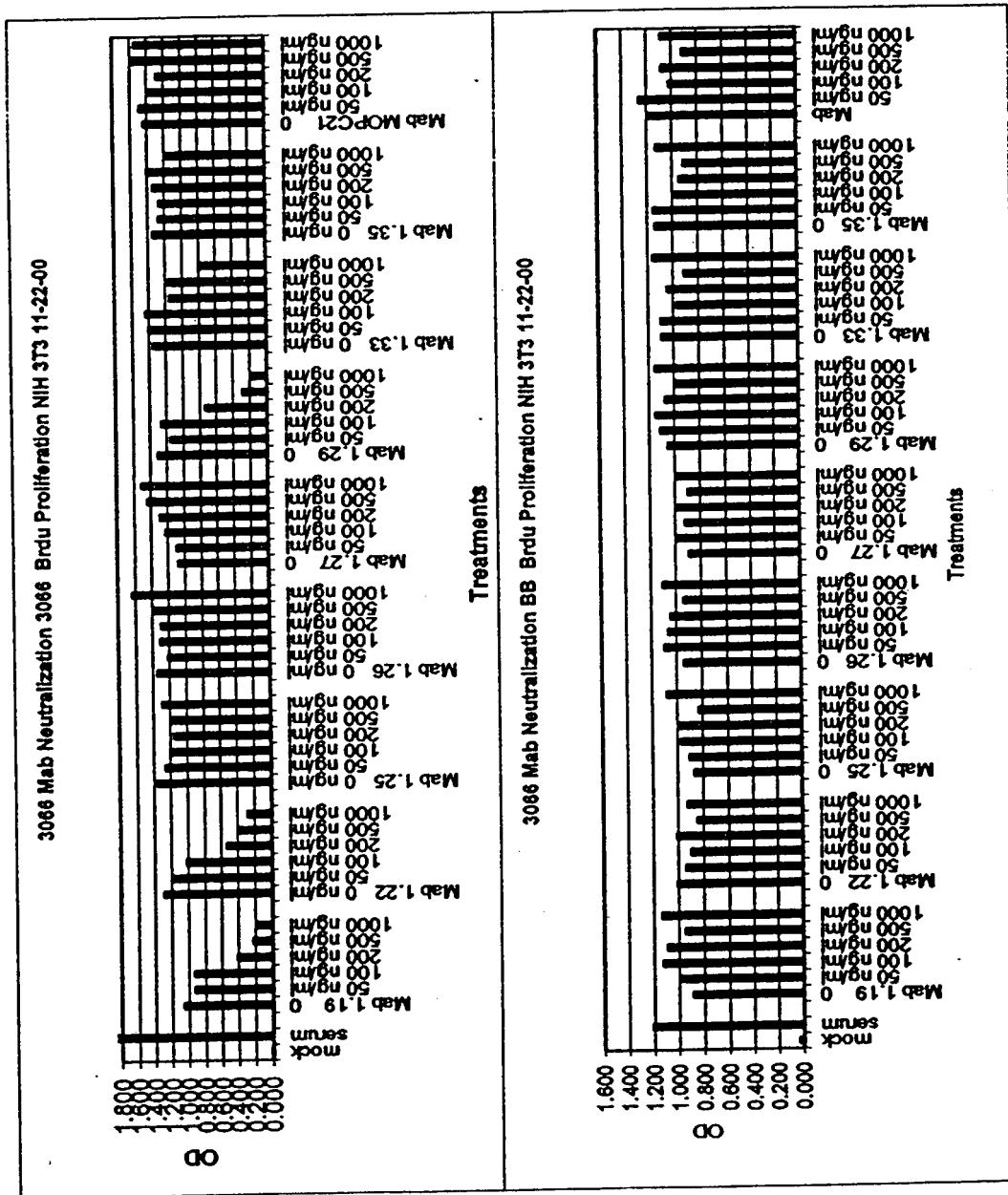




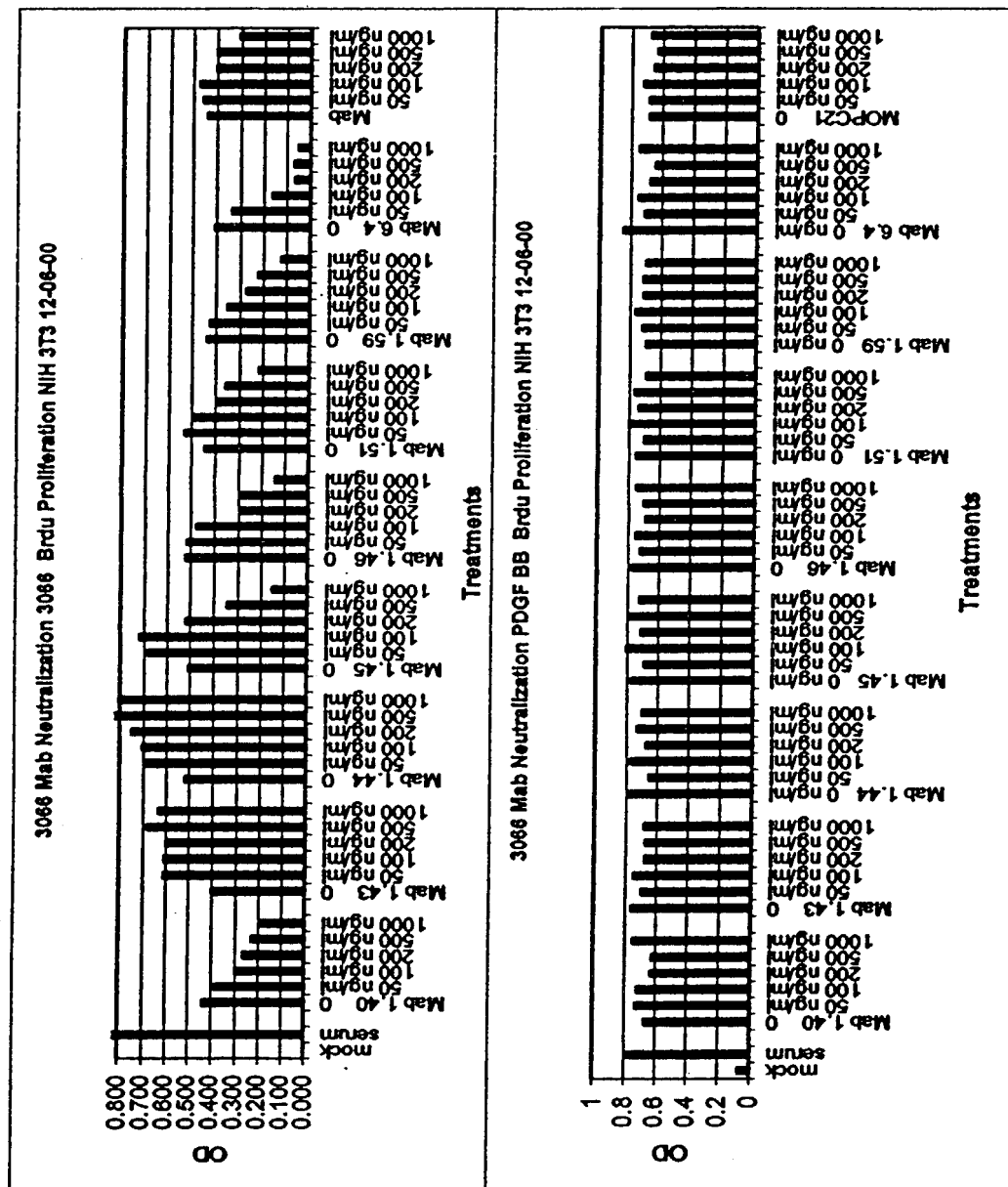
FIGURE 46



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FIGURE 47



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FIGURE 48

1.19 H	1	Q	A	A V V K	T	D N	T Q	WMNPNSGN G	60
6.4 H	1	Q	A	A V V K	T	D N	T Q	WINPNSGN D	60
1.18 H	1	Q	A	A V V K	T	D N	T Q	WMNPNSGN G	60
1.40 H	1	Q	A	A V V K	T	T D N	T Q	WMNPNSGN G	60
1.45 H	1	Q	A	A V V K	T	D N	T Q	WMNPNSGN G	60
1.46 H	1	Q	A	A V V K	S	D N	T Q	WMNPNSGN G	60
1.49 H	1	Q	A	A V V K	T	D N	T Q	WMNPNSGN G	60
1.33 H	1	Q	A	A V V K	T	G S	P Q	WISAYNGN N	60
1.48 H	1	Q	A	A V V K	T	G S	P Q	WISAYNGN N	60
1.6 H	1	E	E GGLV	G LRL A	FN RT	NMN	P K	VSSISSSSSNIY	60
1.17 H	1	Q	E GG VQ	K LRL A	FT S	GMH	P K	VAVIWDGSKNY	60
1.24 H	1	Q	E GG VQ	R LRL A	FS S	GMH	P K	VADIWDGSKNY	60
1.38 H	1	Q	E GG VQ	R LRL A	FT S	GMH	P K	VAVIWDGNDKY	60
1.11 H	1	E	GGLIQ	G LRL A	FTVS	NYMS	P K	VSVIYSGGS- Y	59
1.23 H	1	E	A	E L I EG	S	W G	MP K	IIYPGDS R	60
1.25 H	1	E	A	E L I KG	R	W G	MP K	IIYPGDS R	60
1.29 H	1	E	A	E L I KG	S	W G	MP K	IIYPGDS R	60
1.39 H	1	E	T	E L I KG	R	W G	MP K	IIYPGDS R	60
1.51 H	1	E	A	E L I KG	S	W G	MP K	IIYPGDSDAK	60

[CDR1] [CDR2]

1.19 H	61	QKF	V MTRNT I	MELS	SE	V	--DVM-ITFGGVIVH-YGM V	116
6.4 H	61	QKF	V MTRDT I	MELS	SE	I V	--GFG-YSYN-YD -YGM V	115
1.18 H	61	QKF	V MTRNT I	MELS	SE	V	--EG--IAVAGTY YYGM V	116
1.40 H	61	QKF	V MTRNT L	MELS	SE	V	--DIV-VVVAATN -NGM V	116
1.45 H	61	QKF	V MTRNT I	MELS	SE	V	--GSG-YSYG-YD -YGM V	115
1.46 H	61	QKF	V MTRNT I	MELS	SE	V	--DIV-VVVTATD -YGM V	116
1.49 H	61	QKF	V MTRNT I	MELS	SE	V F	--MRD-IVATSYY FYGM V	117
1.33 H	61	QKL	V MTTDT T	MELR	SD	V	--DHY-YDSSDYL YYGL V	117
1.48 H	61	QKL	V MTTDT T	MELR	SD	V	DVEYY-YDGSYY FDY----	115
1.6 H	61	DSVK	F ISRDNAKNSL	LQMN	AE	V	DIMI---TFG-GIIASFYF Y	116
1.17 H	61	DSVK	F ISRDN KN L	LQMN	AE	V	DQGY---RYA-GY DYGM V	116
1.24 H	61	DSVK	F ISRDN KN L	LQMN	AE	V	DQGY---SYG-YV DYGM V	116
1.38 H	61	DSVK	F VSRDN KN L	LQMN	AE	V	GYYYD---SSD-YL YYGM V	117
1.11 H	60	DSVK	F ISRDN KN L	LQMN	AE	V	GTVTT-----N YYGM V	110
1.23 H	61	SPSF	QV ISADK I	LQWS	KAS	M	HVSY---YYVSGS -NVF Y	116
1.25 H	61	SPSF	QV ISADK I	LQWS	KAS	M	HGSY---YYGSET -NVF Y	116
1.29 H	61	SPSF	QA ISADK I	LQWS	KAS	M	HVDVGATIGGY Y -HGM V	119
1.39 H	61	SPSF	QV ISADK I	LQWS	KAS	M	HGSY---YYNSGS -NVF Y	116
1.51 H	61	SPSF	QV ISADK I	LQWS	KAS	M	HYDY---VWRNYR T-GWF P	116

[CDR3]



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FIGURE 48 (CONT)

1.19 H	117	T	126
6.4 H	116	T	125
1.18 H	117	T	126
1.40 H	117	T	126
1.45 H	116	T	125
1.46 H	117	T	126
1.49 H	118	T	127
1.33 H	118	T	127
1.48 H	116	L	125
1.6 H	117	L	126
1.17 H	117	T	126
1.24 H	117	T	126
1.38 H	118	T	127
1.11 H	111	T	120
1.23 H	117	L	126
1.25 H	117	L	126
1.29 H	120	T	129
1.39 H	117	L	126
1.51 H	117	L	126

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FIGURE 49

1.48 L	1		V		T	SS-----W A	A KL	I Q 55
1.49 L	1	V	L	PVTP EPAS	S S	SLLHSNGYNY D LL	QS QL	LG SRA 60
1.11 L	1	V	L	PVTP EPAS	S S	SLLQSNGYNY D L	QS QL	LG NRA 60
1.29 L	1	V	L	PVTP EPAS	S S	SLLHSNGYNY D L	QS QL	LG NRA 60
1.45 L	1				N	SN-----D A	V KL	T Q 55
1.33 L	1				T	SN-----Y A	V KL	T Q 55
1.38 L	1				T	SN-----Y A	V NL	T Q 55
6.4 L	1	E VL	GT	L P E A	LS	SVSSS-----Y A	QA RL	T SRA 56
1.51 L	1	E VL	GT	L P E A	LS	SVSSS-----Y A	QA RL	G NRA 56
1.19 L	1				T	RN-----D G	A KR	S Q 55
1.18 L	1				T	RN-----D G	A KR	S Q 55
1.16 L	1				T	RN-----D G F	A KR	S Q 55
1.23 L	1				T	RN-----D G	I A KR	S Q 55
1.25 L	1				T	RN-----D G	A KR	S Q 55
1.39 L	1				T	RN-----D G	A KR	S Q 55
1.17 L	1				T	RN-----D G	A KR	S Q 55
1.24 L	1				T	RN-----D G	A KR	S Q 55
1.46 L	1				T	RN-----D G	A KR	F S P 55

[CDR1] [CDR2]

1.48 L	56		D		F S	Q SN F R -	Q	107
1.49 L	61	D	D	K RVEA	VG V	M TLQTIT--	Q RL	111
1.11 L	61	D	D	K RVEA	VG V	M ALQTLT--	G	111
1.29 L	61	D	D	K RVEAD	VG V	M ALQSLMCS	Q L	113
1.45 L	56	L	D		V T	QKYN A F -	P D	107
1.33 L	56		D		V T	QKYN A L -	G	107
1.38 L	56		D S		V A	QKCN A W -	Q T	107
6.4 L	57	T I D	D	R E	F V	Q YG S CS-	Q L	108
1.51 L	57	T I D	D	R E	F V	Q YG SLF -	P D	108
1.19 L	56		D		F T	L HN D CS-	Q L R	107
1.18 L	56		E		F T F	L HN Y F -	P D	107
1.16 L	56		E		F T	L HN Y L -	G	107
1.23 L	56	R	E		F T	L HN Y W -	Q	107
1.25 L	56		E		F T	L HN Y W -	Q	107
1.39 L	56		E		F T	L HN Y W -	Q	107
1.17 L	56		E		F T	L HN Y L -	G	107
1.24 L	56		E		F T	L HN Y W -	Q	107
1.46 L	56		E		F T	L HSGY P -	Q	107

[CDR3]



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FIGURE 51

1.33 H	1								60
1.48 H	1								60
				[CDR1]				[CDR2]	
1.33 H	61							--DH S D L YY GLDV	118
1.48 H	61							DVEY G G Y FD ----	116
								[CDR3]	
1.33 H	119	T							
1.48 H	117	L							



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FIGURE 52

1.17 H 1	K	T	V	SN	60
1.24 H 1	R	S	D	SN	60
1.38 H 1	R	T	I	ND	60
		[CDR1]		[CDR2]	
1.17 H 61	I		DQG -RYAGY	D	119
1.24 H 61	I		DQG -SYGYV	D	119
1.38 H 61	V		GYD DSSDYL	Y	120
			[CDR3]		
1.17 H 120	126				
1.24 H 120	126				
1.38 H 121	127				



FIGURE 54

1.49 L 1	H	L	S 60
1.11 L 1	Q	Q	N 60
1.29 L 1	H	Q	N 60
	[CDR1]		[CDR2]
1.49 L 61	E	T TIT-- Q RL 111	
1.11 L 61	E	A TLT-- G KV 111	
1.29 L 61	D	A SLMCS Q KL 113	
		[CDR3]	



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FIGURE 55

1.45 L 1
1.33 L 1
1.38 L 1

N	D	K	L	60
T	Y	K	S	60
T	Y	N	S	60
[CDR1]		[CDR2]		

1.45 L 61
1.33 L 61
1.38 L 61

T	T	Y	F	P	K	D	107
T	T	Y	L	G	K	E	107
S	A	C	W	Q	T	E	107
	[CDR3]						



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FIGURE 56

6.4 L 1
1.51 L 1

[CDR1]

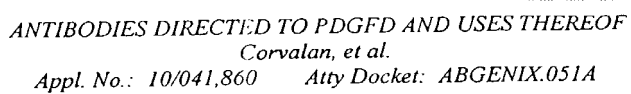
AT S 60
GA N 60

[CDR2]

6.4 L 61
1.51 L 61

PCS Q LE 108
LFT P VD 108

[CDR3]



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[illegible]